GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 18:52:59 ; Search time 75.2941 Seconds
(without alignments)
58.355 Million cell updates/sec

Title: US-09-529-206E-15
Perfect score: 47
Sequence: 1 TVSGNILTIR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	47	100.0	10	2	AAY05980	Aay05980 Human can
2	47	100.0	10	2	AAY05988	Aay05988 Human can
3	47	100.0	14	4	AAE07788	Aae07788 Human NY
4	47	100.0	14	4	AAE07728	Aae07728 Human NY
5	47	100.0	15	4	AAE07726	Aae07726 Human NY
6	47	100.0	15	4	AAE07727	Aae07727 Human NY
7	47	100.0	15	4	AAE07786	Aae07786 Human NY
8	47	100.0	15	4	AAE07787	Aae07787 Human NY
9	47	100.0	18	3	AAY52440	Aay52440 Human tum
10	47	100.0	18	4	AAB69940	Aab69940 Human NY-
11	47	100.0	18	4	AAB69944	Aab69944 Human NY-
12	47	100.0	18	4	AAU01544	Aau01544 HLA-DR53
13	47	100.0	18	4	AAU01540	Aau01540 HLA-DR53
14	47	100.0	18	4	AAE07769	Aae07769 Human NY
15	47	100.0	18	9	ADW50855	Adw50855 NY-ESO-1
16	47	100.0	18	9	ADX08648	Adx08648 Class II
17	47	100.0	20	4	AAE07742	Aae07742 Human ESO
18	47	100.0	20	8	ADI19891	Adi19891 Human HLA
19	47	100.0	20	8	ADI19048	Adi19048 Human HLA
20	47	100.0	20	8	ADJ58397	Adj58397 Peptide p
21	47	100.0	20	9	ADZ67819	Adz67819 Major his
22	47	100.0	25	4	AAE07718	Aae07718 Human NY
23	47	100.0	25	7	ADD71521	Add71521 HLA-DP4 b
24	47	100.0	25	9	ADZ67810	Adz67810 Major his
25	47	100.0	27	4	AAE07717	Aae07717 Human NY
26	47	100.0	30	5	AAU85110	Aau85110 Human NYN
27	47	100.0	36	5	ABG79131	Abg79131 Human NY-
28	47	100.0	54	8	ADG89697	Adg89697 Class II
29	47	100.0	123	8	ADQ10452	Adq10452 Epitope l
30	47	100.0	123	8	ADS80932	Ads80932 DNA plasm
31	47	100.0	179	8	ADK68648	Adk68648 Epitope l
32	47	100.0	179	8	ADK68657	Adk68657 Epitope l
33	47	100.0	179	8	ADQ10455	Adq10455 Epitope l
34	47	100.0	179	8	ADS80935	Ads80935 DNA plasm
35	47	100.0	180	2	AAW62584	Aaw62584 Cancer as
36	47	100.0	180	2	AAW69665	Aaw69665 Human NY-
37	47	100.0	180	2	AAY05965	Aay05965 Human can
38	47	100.0	180	3	AAY52430	Aay52430 Human tum
39	47	100.0	180	3	AAY70862	Aay70862 Human tum
40	47	100.0	180	3	AAB03154	Aab03154 Human oes
41	47	100.0	180	4	AAB69946	Aab69946 Human NY-
42	47	100.0	180	4	AAG67164	Aag67164 Amino aci
43	47	100.0	180	4	AAU01535	Aau01535 Human NY-
44	47	100.0	180	4	AAE07714	Aae07714 Human NY
45	47	100.0	180	5	AAU84818	Aau84818 Human NYN

ALIGNMENTS

RESULT 1
AAY05980
ID AAY05980 standard; peptide; 10 AA.
XX
AC AAY05980;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide ESO10-127.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Claim 17; Page 64; 88pp; English.
XX
CC This sequence represents cancer peptide ESO10-127 that corresponds to
CC amino acid residues 127-136 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
CC AAY05965), a new and potent tumour antigen capable of eliciting an
CC antigen specific immune response by T cells. Cancer peptides derived from
CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
CC variants (see AAY05967-87), are useful as cancer vaccines that protect
CC against cancer. The invention provides: vectors and host cells (also
CC useful as vaccines); a method of diagnosis of cancer or precancer; a
CC transgenic animal; antisense oligonucleotides that inhibit expression of

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CC   the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
CC   cancer peptide, useful in diagnostic and detection assays; and methods
CC   for preventing or inhibiting cancer by administering a cancer peptide,
CC   with or without an HLA molecule. The cancer peptides form part of, or are
CC   derived from, cancers such as primary or metastatic melanoma, thymoma,
CC   lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC   cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC   as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
CC   treated by inducing cancer-specific T cells in vitro for subsequent
CC   return to a patient
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 47;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.004;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          1 TVSGNILTIR 10


RESULT 2
AAY05988
ID   AAY05988 standard; peptide; 10 AA.
XX
AC   AAY05988;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW   NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW   leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW   metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW   uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW   cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW   liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW   vaccine; human leukocyte antigen; HLA.
XX
OS   Homo sapiens.
XX
PN   WO9918206-A2.
XX
PD   15-APR-1999.
XX
PF   21-SEP-1998;   98WO-US019609.
XX
PR   08-OCT-1997;   97US-0061428P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang RF,  Rosenberg SA;
XX
DR   WPI; 1999-277270/23.
XX
PT   Cancer antigen NY ESO1/CAG-3.
XX
PS   Example 10; Page 42; 88pp; English.
XX
CC   This peptide was identified as an HLA peptide motif following a screen
CC   for epitopes from the coding region of human NY ESO-1/CAG-3 ORF1 (see
CC   AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified. The present
CC   peptide (ranked 1) corresponds to amino acid residues 127-136 of CAG-1
CC   ORF1 (see AAY05965). CAG-1 is a new and potent tumour antigen capable of
CC   eliciting an antigen specific immune response by T cells. Cancer peptides
CC   (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their
CC   variants, are useful as cancer vaccines. A claimed method of preventing
CC   or inhibiting cancer involves administering a cancer peptide, with or
CC   without an HLA molecule. The cancer peptides form part of, or are derived
CC   from, cancers such as primary or metastatic melanoma, thymoma, lymphoma,
CC   sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
CC   cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
CC   prostate, ovarian, pancreatic and thyroid cancers
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 47;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.004;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          1 TVSGNILTIR 10


RESULT 3
AAE07788
ID   AAE07788 standard; peptide; 14 AA.
XX
AC   AAE07788;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human NY ESO-1 peptide #22 to characterise epitope recognised by TE4-1.
XX
KW   Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW   class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW   NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW   tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW   immunotherapy.
XX
OS   Homo sapiens.
XX
PN   WO200155393-A2.
XX
PD   02-AUG-2001.
XX
PF   26-JAN-2001; 2001WO-US002765.
XX
PR   28-JAN-2000; 2000US-0179004P.
PR   29-SEP-2000; 2000US-0237107P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang R,  Rosenberg SA,  Zeng G;
XX
DR   WPI; 2001-496851/54.
XX
PT   New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT   useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT   protection from metastasis.
XX
PS   Example 6; Fig 6A; 134pp; English.
XX
CC   The invention relates to the identification and isolation of major
CC   histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC   epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC   from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC   antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC   restricted. The products of the gene are promising candidates for
CC   immunotherapeutic strategies for the prevention, treatment and diagnosis
CC   of patients with cancer. The cancer epitopes are useful as immunogen and
CC   vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC   lymphocytes resulting in protection of the recipient from development of
CC   cancer and protection from metastasis, or by inhibiting the growth of
CC   cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC   useful as diagnostic agent to detect the presence of cancer, to enhance
CC   the generation of antibody and/or CD8+ T cell responses against any given
CC   target antigen and/or hapten and to induce tumour-specific humoral-
CC   mediated immunity against cancer. The present sequence is human NY ESO-1
CC   peptide used in the characterisation of the NY ESO-1 epitope recognised
CC   by TE4-1
XX
SQ   Sequence 14 AA;
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  Query Match           100.0%;  Score 47;  DB 4;  Length 14;
  Best Local Similarity  100.0%;  Pred. No. 0.0061;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          4 TVSGNILTIR 13


RESULT 4
AAE07728
ID   AAE07728 standard; peptide; 14 AA.
XX
AC   AAE07728;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human NY ESO-1 MHC class II restricted T cell epitope #14.
XX
KW   Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW   class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW   NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW   tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW   immunotherapy.
XX
OS   Homo sapiens.
XX
PN   WO200155393-A2.
XX
PD   02-AUG-2001.
XX
PF   26-JAN-2001; 2001WO-US002765.
XX
PR   28-JAN-2000; 2000US-0179004P.
PR   29-SEP-2000; 2000US-0237107P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang R,  Rosenberg SA,  Zeng G;
XX
DR   WPI; 2001-496851/54.
XX
PT   New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT   useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT   protection from metastasis.
XX
PS   Claim 4; Page 16; 134pp; English.
XX
CC   The invention relates to the identification and isolation of major
CC   histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC   epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC   from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC   antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC   restricted. The products of the gene are promising candidates for
CC   immunotherapeutic strategies for the prevention, treatment and diagnosis
CC   of patients with cancer. The cancer epitopes are useful as immunogen and
CC   vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC   lymphocytes resulting in protection of the recipient from development of
CC   cancer and protection from metastasis, or by inhibiting the growth of
CC   cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC   useful as diagnostic agent to detect the presence of cancer, to enhance
CC   the generation of antibody and/or CD8+ T cell responses against any given
CC   target antigen and/or hapten and to induce tumour-specific humoral-
CC   mediated immunity against cancer. The present sequence is MHC class II
CC   restricted T cell epitope of human NY ESO-1 protein
XX
SQ   Sequence 14 AA;

  Query Match           100.0%;  Score 47;  DB 4;  Length 14;
  Best Local Similarity  100.0%;  Pred. No. 0.0061;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          4 TVSGNILTIR 13


RESULT 5
AAE07726
ID   AAE07726 standard; peptide; 15 AA.
XX
AC   AAE07726;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human NY ESO-1 MHC class II restricted T cell epitope #12.
XX
KW   Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW   class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW   NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW   tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW   immunotherapy.
XX
OS   Homo sapiens.
XX
PN   WO200155393-A2.
XX
PD   02-AUG-2001.
XX
PF   26-JAN-2001; 2001WO-US002765.
XX
PR   28-JAN-2000; 2000US-0179004P.
PR   29-SEP-2000; 2000US-0237107P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang R,  Rosenberg SA,  Zeng G;
XX
DR   WPI; 2001-496851/54.
XX
PT   New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT   useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT   protection from metastasis.
XX
PS   Claim 4; Page 16; 134pp; English.
XX
CC   The invention relates to the identification and isolation of major
CC   histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC   epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC   from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC   antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC   restricted. The products of the gene are promising candidates for
CC   immunotherapeutic strategies for the prevention, treatment and diagnosis
CC   of patients with cancer. The cancer epitopes are useful as immunogen and
CC   vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC   lymphocytes resulting in protection of the recipient from development of
CC   cancer and protection from metastasis, or by inhibiting the growth of
CC   cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC   useful as diagnostic agent to detect the presence of cancer, to enhance
CC   the generation of antibody and/or CD8+ T cell responses against any given
CC   target antigen and/or hapten and to induce tumour-specific humoral-
CC   mediated immunity against cancer. The present sequence is MHC class II
CC   restricted T cell epitope of human NY ESO-1 protein
XX
SQ   Sequence 15 AA;

  Query Match           100.0%;  Score 47;  DB 4;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 0.0067;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          6 TVSGNILTIR 15


RESULT 6
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AAE07727
ID   AAE07727 standard; peptide; 15 AA.
XX
AC   AAE07727;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human NY ESO-1 MHC class II restricted T cell epitope #13.
XX
KW   Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW   class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW   NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW   tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW   immunotherapy.
XX
OS   Homo sapiens.
XX
PN   WO200155393-A2.
XX
PD   02-AUG-2001.
XX
PF   26-JAN-2001; 2001WO-US002765.
XX
PR   28-JAN-2000; 2000US-0179004P.
PR   29-SEP-2000; 2000US-0237107P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang R,  Rosenberg SA,  Zeng G;
XX
DR   WPI; 2001-496851/54.
XX
PT   New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT   useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT   protection from metastasis.
XX
PS   Claim 4; Page 16; 134pp; English.
XX
CC   The invention relates to the identification and isolation of major
CC   histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC   epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC   from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC   antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC   restricted. The products of the gene are promising candidates for
CC   immunotherapeutic strategies for the prevention, treatment and diagnosis
CC   of patients with cancer. The cancer epitopes are useful as immunogen and
CC   vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC   lymphocytes resulting in protection of the recipient from development of
CC   cancer and protection from metastasis, or by inhibiting the growth of
CC   cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC   useful as diagnostic agent to detect the presence of cancer, to enhance
CC   the generation of antibody and/or CD8+ T cell responses against any given
CC   target antigen and/or hapten and to induce tumour-specific humoral-
CC   mediated immunity against cancer. The present sequence is MHC class II
CC   restricted T cell epitope of human NY ESO-1 protein
XX
SQ   Sequence 15 AA;

  Query Match             100.0%;  Score 47;  DB 4;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.0067;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          5 TVSGNILTIR 14


RESULT 7
AAE07786
ID   AAE07786 standard; peptide; 15 AA.
XX
AC   AAE07786;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human NY ESO-1 peptide #20 to characterise epitope recognised by TE4-1.
XX
KW   Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW   class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW   NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW   tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW   immunotherapy.
XX
OS   Homo sapiens.
XX
PN   WO200155393-A2.
XX
PD   02-AUG-2001.
XX
PF   26-JAN-2001; 2001WO-US002765.
XX
PR   28-JAN-2000; 2000US-0179004P.
PR   29-SEP-2000; 2000US-0237107P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang R,  Rosenberg SA,  Zeng G;
XX
DR   WPI; 2001-496851/54.
XX
PT   New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT   useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT   protection from metastasis.
XX
PS   Example 6; Fig 6A; 134pp; English.
XX
CC   The invention relates to the identification and isolation of major
CC   histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC   epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC   from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC   antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC   restricted. The products of the gene are promising candidates for
CC   immunotherapeutic strategies for the prevention, treatment and diagnosis
CC   of patients with cancer. The cancer epitopes are useful as immunogen and
CC   vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC   lymphocytes resulting in protection of the recipient from development of
CC   cancer and protection from metastasis, or by inhibiting the growth of
CC   cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC   useful as diagnostic agent to detect the presence of cancer, to enhance
CC   the generation of antibody and/or CD8+ T cell responses against any given
CC   target antigen and/or hapten and to induce tumour-specific humoral-
CC   mediated immunity against cancer. The present sequence is human NY ESO-1
CC   peptide used in the characterisation of the NY ESO-1 epitope recognised
CC   by TE4-1
XX
SQ   Sequence 15 AA;

  Query Match             100.0%;  Score 47;  DB 4;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.0067;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          6 TVSGNILTIR 15


RESULT 8
AAE07787
ID   AAE07787 standard; peptide; 15 AA.
XX
AC   AAE07787;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human NY ESO-1 peptide #21 to characterise epitope recognised by TE4-1.
XX
```

KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US002765.
XX
PR 28-JAN-2000; 2000US-0179004P.
PR 29-SEP-2000; 2000US-0237107P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
DR WPI; 2001-496851/54.
XX
PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis.
XX
PS Example 6; Fig 6A; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any given
CC target antigen and/or hapten and to induce tumour-specific humoral-
CC mediated immunity against cancer. The present sequence is human NY ESO-1
CC peptide used in the characterisation of the NY ESO-1 epitope recognised
CC by TE4-1
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 47; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNILTIR 10
||||||||||
Db 5 TVSGNILTIR 14

RESULT 9
AAY52440
ID AAY52440 standard; protein; 18 AA.
XX
AC AAY52440;
XX
DT 15-FEB-2000 (first entry)
XX
DE Human tumour antigen NY-ESO-1 peptide #13.
XX
KW Cancer; tumour; antigen; MHC; major histocompatility complex; Class II;
KW T-cell; helper; stimulation; proliferation; treatment; diagnosis;
KW prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;
KW hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9953938-A1.
XX
PD 28-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US006875.
XX
PR 17-APR-1998; 98US-00062422.
PR 02-OCT-1998; 98US-00165546.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI Gure A, Ritter G;
XX
DR WPI; 2000-038483/03.
XX
PT Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes.
XX
PS Claim 4; Page 22; 49pp; English.
XX
CC Peptides #8-#13 (AAY52435-Y52440) are peptides derived from the human
CC tumour antigen, NY-ESO-1 (AAY52430) which can bind to MHC(major
CC histocompatibility Class II HLA-DR53 molecules, thereby stimulating
CC proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially
CC isolated from an oesophagus squamous cell cancer cDNA library. Tissue
CC localisation studies revealed it to be expressed at high levels in normal
CC ovary and testis but not in normal colon, kidney, liver, brain,
CC oesophagus and skin. It was expressed in certain tumours and tumour cell
CC lines with some degree of frequency - these included melanoma specimens
CC and cell lines, and breast and bladder cancer specimens, with expression
CC in other tumour types being sporadic. These NY-ESO-1-derived peptides may
CC be used in methods and compositions used for the treatment, diagnosis and
CC prevention of cancers (such as melanoma, breast cancer, prostate cancer,
CC lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or
CC lymphoma) and to stimulate the proliferation of T cells
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 47; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNILTIR 10
||||||||||
Db 1 TVSGNILTIR 10

RESULT 10
AAB69940
ID AAB69940 standard; peptide; 18 AA.
XX
AC AAB69940;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 HLA-DR53 binding motif #2.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US019220.

XX
PR 23-JUL-1999; 99US-00359503.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX
DR WPI; 2001-182822/18.
XX
PT Method useful for determining the status (e.g. progression, regression or
PT stability of the disease) of a cancerous condition, involves determining
PT the levels of NY-ESO-1 specific antibodies in a sample taken from a
PT patient.
XX
PS Example 16; Page 27; 50pp; English.
XX
CC The present sequence is given in a specification relating to a method for
CC determining the status of a cancerous condition in a patient with a
CC tumour that expresses NY-ESO-1. The method comprises assaying a sample
CC taken from the patient for antibodies that specifically bind to the NY-
CC ESO-1 and comparing the value obtained to a prior value obtained from
CC assay of a prior sample taken from the patient. Any difference between
CC the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma, non-small
CC cell lung carcinoma or bladder carcinoma
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNILTIR 10
||||||||||
Db 7 TVSGNILTIR 16

RESULT 11
AAB69944
ID AAB69944 standard; peptide; 18 AA.
XX
AC AAB69944;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 HLA-DR53 binding motif #6.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
OS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US019220.
XX
PR 23-JUL-1999; 99US-00359503.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX
DR WPI; 2001-182822/18.
XX
PT Method useful for determining the status (e.g. progression, regression or
PT stability of the disease) of a cancerous condition, involves determining
PT the levels of NY-ESO-1 specific antibodies in a sample taken from a
PT patient.
XX
PS Example 16; Page 28; 50pp; English.
XX
CC The present sequence is given in a specification relating to a method for
CC determining the status of a cancerous condition in a patient with a
CC tumour that expresses NY-ESO-1. The method comprises assaying a sample
CC taken from the patient for antibodies that specifically bind to the NY-
CC ESO-1 and comparing the value obtained to a prior value obtained from
CC assay of a prior sample taken from the patient. Any difference between
CC the values is indicative of a change in status of the cancerous
CC condition. The method is useful for determining whether a cancerous
CC condition is progressing, regressing or remaining stable, in particular
CC in patients receiving treatment for a melanoma, adenocarcinoma, non-small
CC cell lung carcinoma or bladder carcinoma
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNILTIR 10
||||||||||
Db 1 TVSGNILTIR 10

RESULT 12
AAU01544
ID AAU01544 standard; peptide; 18 AA.
XX
AC AAU01544;
XX
DT 18-JUL-2001 (first entry)
XX
DE HLA-DR53 recognising NY-ESO-1 peptide #6.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX
OS Homo sapiens.
XX
PN WO200123560-A2.
XX
PD 05-APR-2001.
XX
PF 26-SEP-2000; 2000WO-US026411.
XX
PR 29-SEP-1999; 99US-00408036.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Tureci O, Sahin U, Pfreundschuh M;
XX
DR WPI; 2001-266156/27.
XX
PT Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid sequence
PT found in tumor rejection antigen precursor used for stimulating
PT proliferation of helper T cells.
XX
PS Example 13; Page 19; 62pp; English.
XX
CC The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
CC complex (MHC) Class II molecules such as human leukocyte antigen-

CC determining region (HLA-DR) molecules and stimulate proliferation of
CC helper T cells. The peptides can be administered to an HLA-DR positive
CC subject in order to stimulate the helper T cells. An MHC Class II HLA-DR-
CC NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in
CC free form is useful for this stimulation. The nucleic acid is useful for
CC screening for a cancerous condition, which involves contacting a subject
CC sample to a cell line transfected with the immunoreactive cell (helper T
CC cell), where interaction is indicative of cancer. In addition, a sample
CC from a patient (for example, a body fluid or tissue) can be monitored for
CC the amount of the complex present in the bloodstream. This is useful for
CC determining regression, progression or onset of a cancerous condition.
CC The method involves contacting the sample with a radioactive labelled or
CC enzyme labelled monoclonal antibody which specifically binds with the
CC complex
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNILTIR 10
||||||||||
Db 1 TVSGNILTIR 10

RESULT 13
AAU01540
ID AAU01540 standard; peptide; 18 AA.
XX
AC AAU01540;
XX
DT 18-JUL-2001 (first entry)
XX
DE HLA-DR53 recognising NY-ESO-1 peptide #2.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX
OS Homo sapiens.
XX
PN WO200123560-A2.
XX
PD 05-APR-2001.
XX
PF 26-SEP-2000; 2000WO-US026411.
XX
PR 29-SEP-1999; 99US-00408036.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Tureci O, Sahin U, Pfreundschuh M;
XX
DR WPI; 2001-266156/27.
XX
PT Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid sequence
PT found in tumor rejection antigen precursor used for stimulating
PT proliferation of helper T cells.
XX
PS Example 13; Page 19; 62pp; English.
XX
CC The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
CC complex (MHC) Class II molecules such as human leukocyte antigen-
CC determining region (HLA-DR) molecules and stimulate proliferation of
CC helper T cells. The peptides can be administered to an HLA-DR positive
CC subject in order to stimulate the helper T cells. An MHC Class II HLA-DR-
CC NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in
CC free form is useful for this stimulation. The nucleic acid is useful for
CC screening for a cancerous condition, which involves contacting a subject
CC sample to a cell line transfected with the immunoreactive cell (helper T
CC cell), where interaction is indicative of cancer. In addition, a sample
CC from a patient (for example, a body fluid or tissue) can be monitored for
CC the amount of the complex present in the bloodstream. This is useful for
CC determining regression, progression or onset of a cancerous condition.
CC The method involves contacting the sample with a radioactive labelled or
CC enzyme labelled monoclonal antibody which specifically binds with the
CC complex
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNILTIR 10
||||||||||
Db 7 TVSGNILTIR 16

RESULT 14
AAE07769
ID AAE07769 standard; peptide; 18 AA.
XX
AC AAE07769;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 HLA DR restricted T cell cancer peptide #1.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US002765.
XX
PR 28-JAN-2000; 2000US-0179004P.
PR 29-SEP-2000; 2000US-0237107P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
DR WPI; 2001-496851/54.
XX
PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis.
XX
PS Claim 84; Page 84; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also

```
CC   useful as diagnostic agent to detect the presence of cancer, to enhance
CC   the generation of antibody and/or CD8+ T cell responses against any given
CC   target antigen and/or hapten and to induce tumour-specific humoral-
CC   mediated immunity against cancer. The present sequence is human NY ESO-1
CC   HLA DR restricted T cell cancer peptide
XX
SQ   Sequence 18 AA;

  Query Match           100.0%;  Score 47;  DB 4;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 0.0084;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          7 TVSGNILTIR 16


RESULT 15
ADW50855
ID   ADW50855 standard; peptide; 18 AA.
XX
AC   ADW50855;
XX
DT   24-MAR-2005  (first entry)
XX
DE   NY-ESO-1 peptide 121-138.
XX
KW   cytostatic; immune stimulation; cancer; cytostatic; neoplasm; NY-ESO-1.
XX
OS   Unidentified.
XX
PN   WO2005000870-A2.
XX
PD   06-JAN-2005.
XX
PF   27-MAY-2004; 2004WO-US016849.
XX
PR   30-MAY-2003; 2003US-0474893P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
PI   Gnjatic S,  Atanackovic D,  Old LJ;
XX
DR   WPI; 2005-066554/07.
XX
PT   Novel NY-ESO-1 peptide that binds to human leukocyte antigen class II
PT   molecules, useful for treating cancer.
XX
PS   Example 7; Page 12; 24pp; English.
XX
CC   The invention describes an isolated NY-ESO-1 peptide (I), consisting of
CC   amino acids 80-109, 87-98, 108-119, 121-132 or 143-154 of a sequence of
CC   180 (S1) amino acids fully defined in the specification. Also described
CC   are: a composition (II) useful in stimulating a CD4 + T cell response,
CC   comprising (I) and an adjuvant; a composition (III) useful in stimulating
CC   a T cell response in a subject, comprising (I) and at least one
CC   additional peptide; an isolated nucleic acid molecule (IV) consisting of
CC   a nucleotide sequence which encodes a peptide, where the amino acid
CC   sequence is chosen from 80-109, 87-98, 108-119, 121-132 or 143-154 of 180
CC   of (S1); an expression vector (V) comprising (IV) operably linked to a
CC   promoter; a recombinant cell (VI) comprising (IV); a recombinant cell
CC   (VII) comprising (V); and an isolated CD4 + T cell (VIII) which
CC   recognizes a complex of (I) and a major histocompatibility complex (MHC)
CC   Class II molecule. (I) is useful for treating cancer. This is the amino
CC   acid sequence of a NY-ESO-1 peptide.
XX
SQ   Sequence 18 AA;

  Query Match           100.0%;  Score 47;  DB 9;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 0.0084;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          7 TVSGNILTIR 16


Search completed: March 13, 2006, 19:03:56
Job time : 77.2941 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:04:24 ; Search time 11.8824 Seconds
(without alignments)
80.975 Million cell updates/sec

Title: US-09-529-206E-15
Perfect score: 47
Sequence: 1 TVSGNILTIR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	76.6	245	2	T13099	major tail protein
2	36	76.6	323	2	AD2753	lipoic Acid Synthe
3	36	76.6	323	2	B97534	lipoic acid synthe
4	35	74.5	335	2	A89837	hypothetical prote
5	34	72.3	177	1	R5BS0F	ribosomal protein
6	34	72.3	244	2	T41234	translation initia
7	34	72.3	311	2	AB3218	2-hydroxyacid dehy
8	34	72.3	314	2	G86835	hypothetical prote
9	34	72.3	1266	2	A85989	hypothetical prote
10	34	72.3	1266	2	F91143	hypothetical prote
11	33	70.2	144	1	TPBPP1	tail fiber protein
12	33	70.2	144	2	S18683	gene R protein - E
13	33	70.2	411	2	G95241	MATE efflux family
14	33	70.2	426	2	B98106	hypothetical prote
15	33	70.2	428	2	F85253	hypothetical prote
16	33	70.2	436	2	B81033	N-acetylglutamate
17	33	70.2	436	2	A81977	probable amino-aci
18	33	70.2	449	2	S02011	serotonin receptor
19	33	70.2	471	2	A43956	serotonin receptor
20	33	70.2	471	2	S11280	serotonin receptor
21	33	70.2	471	2	S40689	5-hydroxytryptamin
22	33	70.2	471	2	A34863	serotonin receptor
23	33	70.2	876	2	E96674	hypothetical prote
24	33	70.2	918	2	T02759	hypothetical prote
25	33	70.2	1996	2	F71405	probable TMV resis
26	32	68.1	102	2	C86898	hypothetical prote
27	32	68.1	121	2	B81972	probable integral
28	32	68.1	135	2	D81029	conserved hypothet
29	32	68.1	187	2	I37105	5-HT2c receptor -
30	32	68.1	234	2	H75390	hypothetical prote
31	32	68.1	245	2	S57550	hypothetical prote
32	32	68.1	289	2	C87158	probable oxidoredu
33	32	68.1	316	2	S25234	lysozyme (EC 3.2.1
34	32	68.1	344	2	A69325	hypothetical prote
35	32	68.1	347	2	G95146	conserved domain p
36	32	68.1	347	2	E98014	conserved hypothet
37	32	68.1	376	2	C97059	uncharacterized pr
38	32	68.1	418	2	E70401	S-adenosylhomocyst
39	32	68.1	451	2	S65162	hypothetical prote
40	32	68.1	455	1	HMXRS3	sigma 1 protein pr
41	32	68.1	458	2	JS0616	serotonin receptor
42	32	68.1	459	2	A43951	serotonin receptor
43	32	68.1	460	2	A32605	serotonin receptor
44	32	68.1	479	2	S23562	serotonin receptor
45	32	68.1	491	2	T30590	alkylhalidase homo

ALIGNMENTS

RESULT 1
T13099
major tail protein V - phage N15
N;Alternate names: protein gp13
C;Species: phage N15
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13099
R;Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, M.E.; Ravin, N.V.; Smirnov, I.K.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z17603
A;Accession: T13099
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-245 <HEN>
A;Cross-references: UNIPROT:O64327; UNIPARC:UPI000009BA91; EMBL:AF064539; NID:g3192683;
C;Genetics:
A;Note: gene 13
C;Superfamily: phage lambda major tail protein V

Query Match 76.6%; Score 36; DB 2; Length 245;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 TVSGNILTI 9
              ||||| ||:
Db        209 TVSGNTLTV 217
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RESULT 2
AD2753
lipoic Acid Synthetase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 31-Dec-2004
C;Accession: AD2753
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD2753
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-323 <KUR>
A;Cross-references: UNIPROT:Q8UFG1; UNIPARC:UPI000012E6BE; GB:AE008688; PIDN:AAL42442.1
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: lipA
A;Map position: circular chromosome
C;Superfamily: lipoyl synthase

```
  Query Match            76.6%;  Score 36;  DB 2;  Length 323;
  Best Local Similarity   70.0%;  Pred. No. 18;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              || || ||:|
Db        189 TVPGNYLTVR 198


RESULT 3
B97534
lipoic acid synthetase (lip-syn) (lipoate synthase) [imported] - Agrobacterium tumefacie
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 31-Dec-2004
C;Accession: B97534
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: B97534
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-323 <KUR>
A;Cross-references: UNIPROT:Q8UFG1; UNIPARC:UPI000012E6BE; GB:AE007869; PIDN:AAK87227.1;
C;Genetics:
A;Gene: AGR_C_2646
A;Map position: circular chromosome
C;Superfamily: lipoyl synthase

  Query Match            76.6%;  Score 36;  DB 2;  Length 323;
  Best Local Similarity   70.0%;  Pred. No. 18;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              || || ||:|
Db        189 TVPGNYLTVR 198


RESULT 4
A89837
hypothetical protein SA0619 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A89837
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: A89837
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-335 <KUR>
A;Cross-references: UNIPROT:Q99VV7; UNIPARC:UPI00000549A2; GB:BA000018; PID:g13700555; P
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA0619
C;Superfamily: probable sodium-dependent phosphate transporter MTH1885

  Query Match            74.5%;  Score 35;  DB 2;  Length 335;
  Best Local Similarity   70.0%;  Pred. No. 30;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              || |||: ||
Db        245 TVGGNIMKIR 254


RESULT 5
R5BS0F
ribosomal protein L6 - Bacillus stearothermophilus
N;Alternate names: ribosomal protein BL10
C;Species: Bacillus stearothermophilus
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A02766; B39085; S59061
R;Kimura, M.; Rawlings, N.; Appelt, K.
FEBS Lett. 136, 58-64, 1981
A;Title: The amino acid sequence of protein BL10 from the 50S subunit of the Bacillus st
A;Reference number: A02766
A;Accession: A02766
A;Molecule type: protein
A;Residues: 1-177 <KIM>
A;Cross-references: UNIPROT:P02391; UNIPARC:UPI0000050F95
R;Ramakrishnan, V.; Gerchman, S.E.
J. Biol. Chem. 266, 880-885, 1991
A;Title: Cloning, sequencing, and overexpression of genes for ribosomal proteins from Ba
A;Reference number: A39085; MUID:91093287; PMID:1985969
A;Accession: B39085
A;Molecule type: DNA
A;Residues: 8-170 <RAM>
A;Cross-references: UNIPARC:UPI0000173A98; GB:M57622
R;Urlaub, H.; Kruft, V.; Bischof, O.; Mueller, E.C.; Wittmann-Liebold, B.
EMBO J. 14, 4578-4588, 1995
A;Title: Protein-rRNA binding features and their structural and functional implications
A;Reference number: S59051; MUID:96003638; PMID:7556101
A;Accession: S59061
A;Molecule type: protein
A;Residues: 149-163 <URL>
A;Cross-references: UNIPARC:UPI0000173A99
C;Superfamily: ribosomal protein L6/L9
C;Keywords: protein biosynthesis; ribosome

  Query Match            72.3%;  Score 34;  DB 1;  Length 177;
  Best Local Similarity   55.6%;  Pred. No. 24;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTI 9
              || ||::|:
Db         43 TVEGNVITV 51


RESULT 6
T41234
translation initiation factor eIF-6 [imported] - fission yeast (Schizosaccharomyces pomb
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C;Accession: T41234
R;Lyne, M.; Harris, D.E.; Murphey, L.D.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 1999
A;Reference number: Z21979
A;Accession: T41234
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-244 <LYN>
A;Cross-references: UNIPROT:O94476; UNIPARC:UPI000012D3B6; EMBL:AL035075; PIDN:CAA22640
A;Experimental source: strain 972h-; cosmid c1919
C;Genetics:
A;Gene: SPDB:SPCC1919.09
A;Map position: 3
A;Introns: 12/2; 36/2
C;Superfamily: translation initiation factor 6

  Query Match            72.3%;  Score 34;  DB 2;  Length 244;
  Best Local Similarity   75.0%;  Pred. No. 34;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILT 8
              ||:||:||
Db        141 TVAGNVLT 148


RESULT 7
AB3218
```

2-hydroxyacid dehydrogenase Atu5474 [imported] - Agrobacterium tumefaciens (strain C58,
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 05-Oct-2004
C;Accession: AB3218
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB3218
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-311 <KUR>
A;Cross-references: UNIPROT:Q8UJK3; UNIPARC:UPI0000167CD3; GB:AE008687; PIDN:AAL46160.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu5474
A;Genome: plasmid
C;Superfamily: 2-hydroxyacid dehydrogenase

  Query Match 72.3%; Score 34; DB 2; Length 311;
  Best Local Similarity 77.8%; Pred. No. 44;
  Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSGNILTIR 10
 |:|||| |
Db 288 VAGNILTYR 296

RESULT 8
G86835
hypothetical protein yreB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: G86835
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: G86835
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <STO>
A;Cross-references: UNIPROT:Q9CEZ4; UNIPARC:UPI00000D449D; GB:AE005176; PID:g12724702; P
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: yreB

  Query Match 72.3%; Score 34; DB 2; Length 314;
  Best Local Similarity 75.0%; Pred. No. 44;
  Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSGNILTI 9
 :||||||:
Db 93 ISGNILTL 100

RESULT 9
A85989
hypothetical protein Z4604 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: A85989
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85989
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1266 <STO>
A;Cross-references: UNIPROT:Q8X9D5; UNIPARC:UPI00000D082E; GB:AE005174; NID:g12517869;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z4604
C;Superfamily: Escherichia coli hypothetical protein yhdP

  Query Match 72.3%; Score 34; DB 2; Length 1266;
  Best Local Similarity 66.7%; Pred. No. 1.9e+02;
  Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNILTI 9
 |:||| ||:
Db 1017 TISGNTLTL 1025

RESULT 10
F91143
hypothetical protein ECs4118 [imported] - Escherichia coli (strain O157:H7, substrain R
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F91143
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F91143
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1266 <HAY>
A;Cross-references: UNIPROT:Q8X9D5; UNIPARC:UPI00000D082E; GB:BA000007; PIDN:BAB37541.1
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs4118
C;Superfamily: Escherichia coli hypothetical protein yhdP

  Query Match 72.3%; Score 34; DB 2; Length 1266;
  Best Local Similarity 66.7%; Pred. No. 1.9e+02;
  Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNILTI 9
 |:||| ||:
Db 1017 TISGNTLTL 1025

RESULT 11
TPBPP1
tail fiber protein R - phage P1
C;Species: phage P1
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: JS0460
R;Guidolin, A.; Zingg, J.M.; Arber, W.
Gene 76, 239-243, 1989
A;Title: Organization of the bacteriophage P1 tail-fibre operon.
A;Reference number: PS0109; MUID:89326122; PMID:2526777
A;Accession: JS0460
A;Molecule type: DNA
A;Residues: 1-144 <GUI>
A;Cross-references: UNIPROT:P22946; UNIPARC:UPI0000138778; GB:M25470; NID:g341349; PIDN
C;Genetics:
A;Gene: R
C;Superfamily: phage P1 tail fiber protein R
C;Keywords: tail fiber

  Query Match 70.2%; Score 33; DB 1; Length 144;
  Best Local Similarity 60.0%; Pred. No. 31;
  Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TVSGNILTIR 10
 | || |:|:|
Db 79 TYSGGIITVR 88

RESULT 12
S18683
gene R protein - Escherichia coli plasmid p15B
C;Species: Escherichia coli
C;Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S18683
R;Sandmeier, H.; Iida, S.; Huebner, P.; Hiestand-Nauer, R.; Arber, W.
Nucleic Acids Res. 19, 5831-5838, 1991
A;Title: Gene organization in the multiple DNA inversion region Min of plasmid p15B of E
A;Reference number: S18680; MUID:92051368; PMID:1945872
A;Accession: S18683
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-144 <SAN>
A;Cross-references: UNIPROT:Q47426; UNIPARC:UPI00000B4972; EMBL:X62121; NID:g42224; PIDN
C;Genetics:
A;Gene: R
A;Genome: plasmid
C;Superfamily: phage P1 tail fiber protein R

  Query Match 70.2%; Score 33; DB 2; Length 144;
  Best Local Similarity 60.0%; Pred. No. 31;
  Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TVSGNILTIR 10
| || |:|:|
Db 79 TYSGGIITVR 88

RESULT 13
G95241
MATE efflux family protein [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: G95241
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95241
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-411 <KUR>
A;Cross-references: UNIPROT:Q97NG5; UNIPARC:UPI0000051ADC; GB:AE005672; PIDN:AAK76128.1;
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP2065

  Query Match 70.2%; Score 33; DB 2; Length 411;
  Best Local Similarity 66.7%; Pred. No. 94;
  Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNILTI 9
:|:|||:||
Db 30 SVAGNIITI 38

RESULT 14
B98106
hypothetical protein MATE transporter [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: B98106
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: B98106
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-426 <KUR>
A;Cross-references: UNIPROT:Q8DN77; UNIPARC:UPI00000E3724; GB:AE007317; PIDN:AAL00679.1
C;Genetics:
A;Gene: MATE transporter

  Query Match 70.2%; Score 33; DB 2; Length 426;
  Best Local Similarity 66.7%; Pred. No. 98;
  Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNILTI 9
:|:|||:||
Db 45 SVAGNIITI 53

RESULT 15
F85253
hypothetical protein AT4g22170 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
C;Accession: F85253
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprir
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: F85253
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-428 <STO>
A;Cross-references: UNIPROT:Q9SUG4; UNIPARC:UPI00000A1769; GB:NC_001268; NID:g7269062; I
C;Genetics:
A;Gene: AT4g22170
A;Map position: 4
C;Superfamily: F-box containing protein

  Query Match 70.2%; Score 33; DB 2; Length 428;
  Best Local Similarity 60.0%; Pred. No. 98;
  Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNILTIR 10
||:|||| ::
Db 316 TVTGNILRVQ 325

Search completed: March 13, 2006, 19:16:06
Job time : 13.8824 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 18:53:23 ; Search time 72.5882 Seconds
(without alignments)
97.196 Million cell updates/sec

Title: US-09-529-206E-15
Perfect score: 47
Sequence: 1 TVSGNILTIR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	47	100.0	180	1	CTG1B_HUMAN	P78358 homo sapien
2	47	100.0	180	2	Q7LBY4_HUMAN	Q7lby4 homo sapien
3	40	85.1	141	2	Q67QW2_SYMTH	Q67qw2 symbiobacte
4	39	83.0	142	2	Q9NY13_HUMAN	Q9ny13 homo sapien
5	38	80.9	322	1	LIPA_RHIET	O05941 rhizobium e
6	38	80.9	330	2	Q5X5A2_LEGPA	Q5x5a2 legionella
7	38	80.9	617	2	Q4UGM9_THEAN	Q4ugm9 theileria a
8	37	78.7	94	2	Q4UN39_RICFE	Q4un39 rickettsia
9	37	78.7	250	2	Q8G743_BIFLO	Q8g743 bifidobacte
10	37	78.7	330	2	Q5WW87_LEGPL	Q5ww87 legionella
11	37	78.7	334	2	Q5ZVH8_LEGPH	Q5zvh8 legionella
12	37	78.7	1217	2	Q5AFQ7_CANAL	Q5afq7 candida alb
13	36	76.6	245	2	O64327_BPN15	O64327 bacteriopha
14	36	76.6	318	2	Q8EAQ4_SHEON	Q8eaq4 shewanella
15	36	76.6	323	1	LIPA_AGRT5	Q8ufg1 agrobacteri
16	36	76.6	352	2	Q9YHY4_LAMFL	Q9yhy4 lampetra fl
17	36	76.6	450	2	Q9RJ91_STRCO	Q9rj91 streptomyce
18	36	76.6	1115	2	Q4NQF1_9DELT	Q4nqf1 anaeromyxob
19	35	74.5	143	1	ITBA2_HUMAN	Q14657 homo sapien
20	35	74.5	143	2	Q5HY39_HUMAN	Q5hy39 homo sapien
21	35	74.5	144	2	Q8A9J8_BACTN	Q8a9j8 bacteroides
22	35	74.5	334	2	Q4L486_STAHJ	Q4l486 staphylococ
23	35	74.5	335	2	Q6GBG6_STAAS	Q6gbg6 staphylococ
24	35	74.5	335	2	Q6GJ06_STAAR	Q6gj06 staphylococ
25	35	74.5	335	2	Q5HI04_STAAC	Q5hi04 staphylococ
26	35	74.5	335	2	Q7A1K9_STAAW	Q7a1k9 staphylococ
27	35	74.5	335	2	Q932F0_STAAM	Q932f0 staphylococ
28	35	74.5	335	2	Q99VV7_STAAN	Q99vv7 staphylococ
29	35	74.5	336	2	Q5HR76_STAEQ	Q5hr76 staphylococ
30	35	74.5	336	2	Q8CQ35_STAEP	Q8cq35 staphylococ
31	35	74.5	366	2	Q4SDU8_TETNG	Q4sdu8 tetraodon n
32	35	74.5	391	2	Q6LJS0_PHOPR	Q6ljs0 photobacter
33	35	74.5	430	2	Q5WWD6_LEGPL	Q5wwd6 legionella
34	35	74.5	430	2	Q5X554_LEGPA	Q5x554 legionella
35	35	74.5	430	2	Q5ZVD1_LEGPH	Q5zvd1 legionella
36	35	74.5	439	1	TOLB_SILPO	Q5lnu4 silicibacte
37	35	74.5	528	2	Q5LEA1_BACFN	Q5lea1 bacteroides
38	35	74.5	674	2	Q9PT82_XENLA	Q9pt82 xenopus lae
39	35	74.5	674	2	Q9PT83_XENLA	Q9pt83 xenopus lae
40	35	74.5	674	2	Q6IRP9_XENLA	Q6irp9 xenopus lae
41	35	74.5	674	2	Q6NX22_XENTR	Q6nx22 xenopus tro
42	35	74.5	742	2	Q8T4D0_DROME	Q8t4d0 drosophila
43	35	74.5	742	2	Q9VS00_DROME	Q9vs00 drosophila
44	35	74.5	907	2	Q9NEG0_DROME	Q9neg0 drosophila
45	35	74.5	947	2	Q93FV1_9BACE	Q93fv1 bacteroides

ALIGNMENTS

```
RESULT 1
CTG1B_HUMAN
ID   CTG1B_HUMAN    STANDARD;      PRT;   180 AA.
AC   P78358;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-
DE   ESO-1).
GN   Name=CTAG1B; Synonyms=CTAG, CTAG1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
RA   Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,
RA   Williamson B., Stockert E., Pfreundschuh M., Old L.J.;
RT   "A testicular antigen aberrantly expressed in human cancers detected
RT   by autologous antibody screening.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Melanoma;
RX   MEDLINE=98289662; PubMed=9626360;
RA   Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA   de Plaen E., Boon T.;
RT   "LAGE-1, a new gene with tumor specificity.";
RL   Int. J. Cancer 76:903-908(1998).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98430682; PubMed=9759882;
RA   Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,
RA   Schwartzentruber D.J., Rosenberg S.A.;
RT   "A breast and melanoma-shared tumor antigen: T cell responses to
RT   antigenic peptides translated from different open reading frames.";
RL   J. Immunol. 161:3596-3606(1998).
CC   -!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide
CC       variety of cancers. Detected in uterine myometrium.
CC   -!- SIMILARITY: Belongs to the CTAG family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; U87459; AAB49693.1; -; mRNA.
DR   EMBL; AJ003149; CAA05908.1; -; mRNA.
DR   EMBL; AF038567; AAD05202.1; -; mRNA.
DR   HGNC; HGNC:2491; CTAG1B.
DR   MIM; 300156; -.
```

```
KW   Antigen; Transmembrane.
FT   TRANSMEM    156    172       Potential.
FT   COMPBIAS      5     82       Gly-rich.
SQ   SEQUENCE   180 AA;  17992 MW;  B122C5C2C8BE1569 CRC64;

  Query Match             100.0%;  Score 47;  DB 1;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.55;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db        127 TVSGNILTIR 136


RESULT 2
Q7LBY4_HUMAN
ID   Q7LBY4_HUMAN PRELIMINARY;      PRT;   180 AA.
AC   Q7LBY4;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
DE   antigen 1-A).
GN   Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21303268;
RA   Galgoczy P., Rosenthal A., Platzer M.;
RT   "Human-mouse comparative sequence analysis of the NEMO gene reveals an
RT   alternative promoter within the neighboring G6PD gene.";
RL   Gene 271:93-98(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21566154; PubMed=11709543; DOI=10.1093/hmg/10.22.2557;
RA   Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
RA   Patlan H., Ciccodicola A., Kenwrick S., Platzer M., D'Urso M.,
RA   Nelson D.L.;
RT   "Multiple pathogenic and benign genomic rearrangements occur at a 35
RT   kb duplication involving the NEMO and LAGE2 genes.";
RL   Hum. Mol. Genet. 10:2557-2567(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Platzer M.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Platzer M.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RA   Galgoczy P., Platzer M.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99454989; PubMed=10523621;
RA   De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
RT   "DNA methylation is the primary silencing mechanism for a set of germ
RT   line- and tumor-specific genes with a CpG-rich promoter.";
RL   Mol. Cell. Biol. 19:7327-7335(1999).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RA   Lethe B.G.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF277315; AAL27014.1; -; Genomic_DNA.
DR   EMBL; AJ275977; CAB76943.1; -; Genomic_DNA.
DR   EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
SQ   SEQUENCE   180 AA;  17992 MW;  B122C5C2C8BE1569 CRC64;

  Query Match             100.0%;  Score 47;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.55;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db        127 TVSGNILTIR 136


RESULT 3
Q67QW2_SYMTH
ID   Q67QW2_SYMTH PRELIMINARY;      PRT;   141 AA.
AC   Q67QW2;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hsp20 family heat shock protein.
GN   OrderedLocusNames=STH946;
OS   Symbiobacterium thermophilum.
OC   Bacteria; Actinobacteria; Symbiobacterium.
OX   NCBI_TaxID=2734;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=T / IAM 14863;
RX   PubMed=15383646; DOI=10.1093/nar/gkh830;
RA   Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
RA   Morimura K., Ikeda H., Hattori M., Beppu T.;
RT   "Genome sequence of Symbiobacterium thermophilum, an uncultivable
RT   bacterium that depends on microbial commensalism.";
RL   Nucleic Acids Res. 32:4937-4944(2004).
CC   -!- SIMILARITY: Belongs to the small heat shock protein (HSP20)
CC       family.
DR   EMBL; AP006840; BAD39931.1; -; Genomic_DNA.
DR   GO; GO:0006457; P:protein folding; IEA.
DR   GO; GO:0006986; P:response to unfolded protein; IEA.
DR   InterPro; IPR002068; Hsp20.
DR   Pfam; PF00011; HSP20; 1.
DR   PROSITE; PS01031; HSP20; 1.
KW   Complete proteome; Heat shock.
SQ   SEQUENCE   141 AA;  15725 MW;  C7BA8A8CFC50FD36 CRC64;

  Query Match             85.1%;  Score 40;  DB 2;  Length 141;
  Best Local Similarity   80.0%;  Pred. No. 11;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              || ||:||||
Db         67 TVDGNMLTIR 76


RESULT 4
Q9NY13_HUMAN
ID   Q9NY13_HUMAN PRELIMINARY;      PRT;   142 AA.
AC   Q9NY13;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical protein LAGE-2 (Fragment).
GN   Name=LAGE-2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lethe B.G.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ275978; CAB76945.1; -; mRNA.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   142 AA;  13895 MW;  27EBE922AC4ACC7B CRC64;
```

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  Query Match           83.0%;  Score 39;  DB 2;  Length 142;
  Best Local Similarity   88.9%;  Pred. No. 17;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTI 9
              ||||||||:
Db        101 TVSGNILTM 109


RESULT 5
LIPA_RHIET
ID   LIPA_RHIET     STANDARD;      PRT;   322 AA.
AC   O05941;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Lipoyl synthase (EC 2.8.1.-) (Lipoic acid synthase) (Lipoate synthase)
DE   (Lipoyl-acyl-carrier protein synthase) (Sulfur insertion protein lipA)
DE   (Lip-syn).
GN   Name=lipA;
OS   Rhizobium etli.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Rhizobiaceae; Rhizobium.
OX   NCBI_TaxID=29449;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC   STRAIN=CE3;
RX   MEDLINE=97286510; PubMed=9141657; DOI=10.1016/S0378-1097(97)00069-4;
RA   Tate R., Riccio A., Iaccarino M., Patriarca E.J.;
RT   "Cloning and transcriptional analysis of the lipA (lipoic acid
RT   synthetase) gene from Rhizobium etli.";
RL   FEMS Microbiol. Lett. 149:165-172(1997).
CC   -!- FUNCTION: Catalyzes the radical-mediated insertion of two sulfur
CC       atoms into an octanoyl group bound to acyl carrier protein (ACP)
CC       to produce a lipoyl group (By similarity).
CC   -!- CATALYTIC ACTIVITY: octanoyl-[acyl-carrier protein] + 2 sulfurs =
CC       lipoyl-[acyl-carrier protein].
CC   -!- COFACTOR: Binds 1 4Fe-4S cluster coordinated with 3 cysteines and
CC       an exchangeable S-adenosyl-L-methionine (By similarity).
CC   -!- COFACTOR: Binds 1 3Fe-4S cluster (Potential).
CC   -!- PATHWAY: Lipoate biosynthesis; sulfur-insertion step.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: Belongs to the biotin and lipoic acid synthetases
CC       family. LipA subfamily.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; Y11708; CAA72400.1; -; Genomic_DNA.
DR   HAMAP; MF_00206; -; 1.
DR   InterPro; IPR006638; Elp3/MiaB/NifB.
DR   InterPro; IPR003698; Lipoate_synth.
DR   InterPro; IPR007197; Radical_SAM.
DR   PANTHER; PTHR10949; Lipoate_synth; 1.
DR   Pfam; PF04055; Radical_SAM; 1.
DR   PIRSF; PIRSF005963; Lipoyl_synth; 1.
DR   SMART; SM00729; Elp3; 1.
DR   TIGRFAMs; TIGR00510; lipA; 1.
KW   3Fe-4S; 4Fe-4S; Iron; Iron-sulfur; Metal-binding; Transferase.
FT   METAL        61     61       Iron-sulfur 1 (3Fe-4S) (Potential).
FT   METAL        66     66       Iron-sulfur 1 (3Fe-4S) (Potential).
FT   METAL        72     72       Iron-sulfur 1 (3Fe-4S) (Potential).
FT   METAL        87     87       Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By
FT                                similarity).
FT   METAL        91     91       Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By
FT                                similarity).
FT   METAL        94     94       Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By
FT                                similarity).
SQ   SEQUENCE   322 AA;  36298 MW;  45E7185215486847 CRC64;

  Query Match           80.9%;  Score 38;  DB 1;  Length 322;
  Best Local Similarity   70.0%;  Pred. No. 61;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||:|| ||:|
Db        188 TVAGNYLTVR 197


RESULT 6
Q5X5A2_LEGPA
ID   Q5X5A2_LEGPA PRELIMINARY;      PRT;   330 AA.
AC   Q5X5A2;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=lpp1418;
OS   Legionella pneumophila (strain Paris).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC   Legionellaceae; Legionella.
OX   NCBI_TaxID=297246;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15467720; DOI=10.1038/ng1447;
RA   Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA   Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA   Etienne J., Glaser P., Buchrieser C.;
RT   "Evidence in the Legionella pneumophila genome for exploitation of
RT   host cell functions and high genome plasticity.";
RL   Nat. Genet. 36:1165-1173(2004).
DR   EMBL; CR628336; CAH12569.1; -; Genomic_DNA.
DR   LegioList; lpp1418; -.
DR   GO; GO:0050660; F:FAD binding; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0008033; P:tRNA processing; IEA.
DR   InterPro; IPR001269; Du_synth.
DR   Pfam; PF01207; Dus; 1.
DR   PROSITE; PS01136; UPF0034; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   330 AA;  37270 MW;  9BCB4B74CD8BB383 CRC64;

  Query Match           80.9%;  Score 38;  DB 2;  Length 330;
  Best Local Similarity   77.8%;  Pred. No. 63;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTI 9
              |::||||||
Db        204 TINGNILTI 212


RESULT 7
Q4UGM9_THEAN
ID   Q4UGM9_THEAN PRELIMINARY;      PRT;   617 AA.
AC   Q4UGM9;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Theileria parva Tpr-related protein, putative.
GN   ORFNames=TA21390;
OS   Theileria annulata.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC   Theileria.
OX   NCBI_TaxID=5874;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Ankara isolate clone C9;
RA   Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
RA   Hall N., Barrell B.G.;
RT   "The chromosome 1 sequence of Theileria annulata.";
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR940347; CAI73760.1; -; Genomic_DNA.
SQ   SEQUENCE   617 AA;  67272 MW;  2A3696230D209B70 CRC64;
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  Query Match             80.9%;  Score 38;  DB 2;  Length 617;
  Best Local Similarity   70.0%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              |:||| |||:
Db        451 TISGNTLTIK 460


RESULT 8
Q4UN39_RICFE
ID   Q4UN39_RICFE PRELIMINARY;      PRT;    94 AA.
AC   Q4UN39;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=RF_0168;
OS   Rickettsia felis (Rickettsia azadi).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC   Rickettsiaceae; Rickettsieae; Rickettsia; spotted fever group.
OX   NCBI_TaxID=42862;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=URRWXCal2;
RX   PubMed=15984913; DOI=10.1371/journal.pbio.0030248;
RA   Ogata H., Renesto P., Audic S., Robert C., Blanc G., Fournier P.-E.,
RA   Parinello H., Claverie J.-M., Raoult D.;
RT   "The genome sequence of Rickettsia felis identifies the first putative
RT   conjugative plasmid in an obligate intracellular parasite.";
RL   PLoS Biol. 3:E248-E248(2005).
DR   EMBL; CP000053; AAY61019.1; -; Genomic_DNA.
DR   InterPro; IPR007460; DUF497.
DR   Pfam; PF04365; DUF497; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   94 AA;  11378 MW;  D62F3C1DE3CF686E CRC64;

  Query Match             78.7%;  Score 37;  DB 2;  Length 94;
  Best Local Similarity   77.8%;  Pred. No. 28;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 VSGNILTIR 10
              | |||||:|
Db         56 VDGNILTVR 64


RESULT 9
Q8G743_BIFLO
ID   Q8G743_BIFLO PRELIMINARY;      PRT;   250 AA.
AC   Q8G743;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Possible cobyric acid synthase CobQ.
GN   OrderedLocusNames=BL0429;
OS   Bifidobacterium longum.
OC   Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC   Bifidobacteriaceae; Bifidobacterium.
OX   NCBI_TaxID=216816;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=NCC 2705;
RX   MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
RA   Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA   Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
RA   Pridmore R.D., Arigoni F.;
RT   "The genome sequence of Bifidobacterium longum reflects its adaptation
RT   to the human gastrointestinal tract.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR   EMBL; AE014295; AAN24266.1; -; Genomic_DNA.
DR   GO; GO:0003824; F:catalytic activity; IEA.
DR   GO; GO:0009236; P:cobalamin biosynthesis; IEA.
DR   InterPro; IPR011698; GATase_3.
DR   Pfam; PF07685; GATase_3; 1.
KW   Complete proteome.
SQ   SEQUENCE   250 AA;  27653 MW;  7577954A609689CF CRC64;

  Query Match             78.7%;  Score 37;  DB 2;  Length 250;
  Best Local Similarity   87.5%;  Pred. No. 75;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 SGNILTIR 10
              |||:||||
Db         21 SGNVLTIR 28


RESULT 10
Q5WW87_LEGPL
ID   Q5WW87_LEGPL PRELIMINARY;      PRT;   330 AA.
AC   Q5WW87;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=lpl1566;
OS   Legionella pneumophila (strain Lens).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC   Legionellaceae; Legionella.
OX   NCBI_TaxID=297245;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15467720; DOI=10.1038/ng1447;
RA   Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA   Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA   Etienne J., Glaser P., Buchrieser C.;
RT   "Evidence in the Legionella pneumophila genome for exploitation of
RT   host cell functions and high genome plasticity.";
RL   Nat. Genet. 36:1165-1173(2004).
DR   EMBL; CR628337; CAH15806.1; -; Genomic_DNA.
DR   LegioList; lpl1566; -.
DR   GO; GO:0050660; F:FAD binding; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0008033; P:tRNA processing; IEA.
DR   InterPro; IPR001269; Du_synth.
DR   Pfam; PF01207; Dus; 1.
DR   PROSITE; PS01136; UPF0034; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   330 AA;  37311 MW;  BEF836DAF152E15E CRC64;

  Query Match             78.7%;  Score 37;  DB 2;  Length 330;
  Best Local Similarity   66.7%;  Pred. No. 1e+02;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTI 9
              |::|||||:
Db        204 TINGNILTV 212


RESULT 11
Q5ZVH8_LEGPH
ID   Q5ZVH8_LEGPH PRELIMINARY;      PRT;   334 AA.
AC   Q5ZVH8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Zinc binding TIM barrel protein, YjbN family.
GN   OrderedLocusNames=lpg1462;
OS   Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /
OS   ATCC 33152).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC   Legionellaceae; Legionella.
OX   NCBI_TaxID=272624;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15448271; DOI=10.1126/science.1099776;
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RA   Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
RA   Asamani G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J.,
RA   Steshenko V., Park S.H., Zhao B., Teplitskaya E., Edwards J.R.,
RA   Pampou S., Georghiou A., Chou I.-C., Iannuccilli W., Ulz M.E.,
RA   Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
RA   Segal G., Qu X., Rzhetsky A., Zhang P., Cayanis E., De Jong P.J.,
RA   Ju J., Kalachikov S., Shuman H.A., Russo J.J.;
RT   "The genomic sequence of the accidental pathogen Legionella
RT   pneumophila.";
RL   Science 305:1966-1968(2004).
DR   EMBL; AE017354; AAU27544.1; -; Genomic_DNA.
DR   GO; GO:0050660; F:FAD binding; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0008033; P:tRNA processing; IEA.
DR   InterPro; IPR001269; Du_synth.
DR   Pfam; PF01207; Dus; 1.
DR   PROSITE; PS01136; UPF0034; 1.
KW   Complete proteome.
SQ   SEQUENCE   334 AA;  37796 MW;  4B216C11814E0ADD CRC64;

  Query Match             78.7%;  Score 37;  DB 2;  Length 334;
  Best Local Similarity   66.7%;  Pred. No. 1e+02;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTI 9
              |::|||||:
Db        208 TINGNILTV 216


RESULT 12
Q5AFQ7_CANAL
ID   Q5AFQ7_CANAL PRELIMINARY;      PRT;  1217 AA.
AC   Q5AFQ7;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=CaO19.7011;
OS   Candida albicans SC5314.
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX   NCBI_TaxID=237561;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=SC5314;
RX   PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA   Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA   Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA   Davis R.W., Scherer S.;
RT   "The diploid genome sequence of Candida albicans.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=SC5314;
RA   Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA   Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA   Jones T., Scherer S., Agabian N.;
RT   "Annotation of the Genome of Candida albicans.";
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
DR   EMBL; AACQ01000024; EAL01458.1; -; Genomic_DNA.
DR   InterPro; IPR011989; ARM-like.
DR   InterPro; IPR012978; DUF_NUC173.
DR   InterPro; IPR000357; HEAT.
DR   Pfam; PF02985; HEAT; 2.
DR   Pfam; PF08161; NUC173; 1.
KW   Hypothetical protein; Transmembrane.
SQ   SEQUENCE   1217 AA;  135897 MW;  1F2788D13CAD6DEC CRC64;

  Query Match             78.7%;  Score 37;  DB 2;  Length 1217;
  Best Local Similarity   66.7%;  Pred. No. 3.7e+02;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

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              |::|||||:
Db        636 TIAGNILTV 644


RESULT 13
O64327_BPN15
ID   O64327_BPN15 PRELIMINARY;      PRT;  245 AA.
AC   O64327;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Gp13.
GN   Name=gene 13;
OS   Bacteriophage N15.
OC   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC   N15-like viruses.
OX   NCBI_TaxID=40631;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Hendrix R.W., Ravin V.K., Casjens S.R., Ford M.E., Ravin N.V.,
RA   Smirnov I.K.;
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF064539; AAC19050.1; -; Genomic_DNA.
DR   PIR; T13099; T13099.
DR   InterPro; IPR003343; Big_2.
DR   Pfam; PF02368; Big_2; 1.
DR   SMART; SM00635; BID_2; 1.
SQ   SEQUENCE   245 AA;  25571 MW;  2CC941997C103FD3 CRC64;

  Query Match             76.6%;  Score 36;  DB 2;  Length 245;
  Best Local Similarity   77.8%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTI 9
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Db        209 TVSGNTLTV 217


RESULT 14
Q8EAQ4_SHEON
ID   Q8EAQ4_SHEON PRELIMINARY;      PRT;  318 AA.
AC   Q8EAQ4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein SO3842.
GN   OrderedLocusNames=SO3842;
OS   Shewanella oneidensis.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC   Shewanellaceae; Shewanella.
OX   NCBI_TaxID=70863;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=MR-1;
RX   MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA   Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA   Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA   Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
RA   Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA   Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA   White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA   Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA   Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA   Venter J.C., Nealson K.H., Fraser C.M.;
RT   "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT   Shewanella oneidensis.";
RL   Nat. Biotechnol. 20:1118-1123(2002).
DR   EMBL; AE015817; AAN56819.1; -; Genomic_DNA.
DR   TIGR; SO3842; -.
KW   Complete proteome.
SQ   SEQUENCE   318 AA;  34113 MW;  0A0B7165033B6FCF CRC64;
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  Query Match             76.6%;  Score 36;  DB 2;  Length 318;
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Qy          1 TVSGNILT 8
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Db        153 TVSGNIIT 160


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LIPA_AGRT5
ID   LIPA_AGRT5     STANDARD;      PRT;   323 AA.
AC   Q8UFG1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Lipoyl synthase (EC 2.8.1.-) (Lipoic acid synthase) (Lipoate synthase)
DE   (Lipoyl-acyl-carrier protein synthase) (Sulfur insertion protein lipA)
DE   (Lip-syn).
GN   Name=lipA; OrderedLocusNames=Atu1436, AGR_C_2646;
OS   Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Rhizobiaceae; Agrobacterium.
OX   NCBI_TaxID=176299;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA   Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA   Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA   Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA   Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA   Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA   Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA   Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA   Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA   Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA   Nester E.W.;
RT   "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT   C58.";
RL   Science 294:2317-2323(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA   Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA   Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA   Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA   Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA   Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA   Cielo C., Slater S.;
RT   "Genome sequence of the plant pathogen and biotechnology agent
RT   Agrobacterium tumefaciens C58.";
RL   Science 294:2323-2328(2001).
CC   -!- FUNCTION: Catalyzes the radical-mediated insertion of two sulfur
CC       atoms into an octanoyl group bound to acyl carrier protein (ACP)
CC       to produce a lipoyl group (By similarity).
CC   -!- CATALYTIC ACTIVITY: octanoyl-[acyl-carrier protein] + 2 sulfurs =
CC       lipoyl-[acyl-carrier protein].
CC   -!- COFACTOR: Binds 1 4Fe-4S cluster coordinated with 3 cysteines and
CC       an exchangeable S-adenosyl-L-methionine (By similarity).
CC   -!- COFACTOR: Binds 1 3Fe-4S cluster (Potential).
CC   -!- PATHWAY: Lipoate biosynthesis; sulfur-insertion step.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC   -!- SIMILARITY: Belongs to the biotin and lipoic acid synthetases
CC       family. LipA subfamily.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; AE009104; AAL42442.1; -; Genomic_DNA.
DR   EMBL; AE008069; AAK87227.1; -; Genomic_DNA.
DR   PIR; AD2753; AD2753.
DR   PIR; B97534; B97534.
DR   HAMAP; MF_00206; -; 1.
DR   InterPro; IPR006638; Elp3/MiaB/NifB.
DR   InterPro; IPR003698; Lipoate_synth.
DR   InterPro; IPR007197; Radical_SAM.
DR   PANTHER; PTHR10949; Lipoate_synth; 1.
DR   Pfam; PF04055; Radical_SAM; 1.
DR   PIRSF; PIRSF005963; Lipoyl_synth; 1.
DR   SMART; SM00729; Elp3; 1.
DR   TIGRFAMs; TIGR00510; lipA; 1.
KW   3Fe-4S; 4Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding;
KW   Transferase.
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FT   METAL        66     66       Iron-sulfur 1 (3Fe-4S) (Potential).
FT   METAL        72     72       Iron-sulfur 1 (3Fe-4S) (Potential).
FT   METAL        87     87       Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By
FT                                similarity).
FT   METAL        91     91       Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By
FT                                similarity).
FT   METAL        94     94       Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By
FT                                similarity).
SQ   SEQUENCE   323 AA;  36341 MW;  74B294773BC784D2 CRC64;

  Query Match             76.6%;  Score 36;  DB 1;  Length 323;
  Best Local Similarity   70.0%;  Pred. No. 1.5e+02;
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Db        189 TVPGNYLTVR 198


Search completed: March 13, 2006, 19:14:21
Job time : 75.5882 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:14:49 ; Search time 18.5882 Seconds
(without alignments)
44.477 Million cell updates/sec

Title: US-09-529-206E-15
Perfect score: 47
Sequence: 1 TVSGNILTIR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	47	100.0	18	2	US-09-359-503-9	Sequence 9, Appli
2	47	100.0	18	2	US-09-359-503-13	Sequence 13, Appl
3	47	100.0	18	2	US-09-165-546D-9	Sequence 9, Appli
4	47	100.0	18	2	US-09-165-546D-13	Sequence 13, Appl
5	47	100.0	18	2	US-09-408-036B-8	Sequence 8, Appli
6	47	100.0	18	2	US-09-408-036B-12	Sequence 12, Appl
7	47	100.0	180	1	US-08-791-495-9	Sequence 9, Appli
8	47	100.0	180	2	US-08-937-263B-8	Sequence 8, Appli
9	47	100.0	180	2	US-09-751-798-8	Sequence 8, Appli
10	47	100.0	180	2	US-09-392-714-25	Sequence 25, Appl
11	47	100.0	180	2	US-09-165-546D-15	Sequence 15, Appl
12	47	100.0	180	2	US-09-341-829A-9	Sequence 9, Appli
13	47	100.0	180	2	US-09-849-602-30	Sequence 30, Appl
14	42	89.4	9	2	US-09-344-040C-125	Sequence 125, App
15	42	89.4	9	2	US-09-833-039A-125	Sequence 125, App
16	38	80.9	9	2	US-09-344-040C-120	Sequence 120, App
17	38	80.9	9	2	US-09-833-039A-120	Sequence 120, App
18	38	80.9	180	1	US-08-791-495-7	Sequence 7, Appli
19	38	80.9	180	2	US-09-341-829A-7	Sequence 7, Appli
20	37	78.7	574	2	US-09-248-796A-16162	Sequence 16162, A
21	35	74.5	342	2	US-09-134-001C-5428	Sequence 5428, Ap
22	34	72.3	149	2	US-09-540-236-2614	Sequence 2614, Ap
23	34	72.3	177	2	US-09-732-210-1076	Sequence 1076, Ap
24	34	72.3	185	2	US-09-270-767-58027	Sequence 58027, A
25	34	72.3	379	2	US-09-270-767-42707	Sequence 42707, A
26	34	72.3	585	2	US-10-104-047-2739	Sequence 2739, Ap
27	33	70.2	97	1	US-08-118-270-329	Sequence 329, App
28	33	70.2	97	4	PCT-US93-08528-329	Sequence 329, App
29	33	70.2	109	2	US-09-341-461-35	Sequence 35, Appl
30	33	70.2	362	2	US-09-134-001C-5209	Sequence 5209, Ap
31	33	70.2	379	1	US-08-118-270-32	Sequence 32, Appl
32	33	70.2	379	4	PCT-US93-08528-32	Sequence 32, Appl
33	33	70.2	426	2	US-09-583-110-4783	Sequence 4783, Ap
34	33	70.2	426	2	US-09-769-787-34	Sequence 34, Appl
35	33	70.2	434	2	US-09-107-433-3247	Sequence 3247, Ap
36	33	70.2	470	2	US-09-292-071-25	Sequence 25, Appl
37	33	70.2	470	2	US-09-292-069A-25	Sequence 25, Appl
38	33	70.2	470	2	US-09-767-013-25	Sequence 25, Appl
39	33	70.2	470	2	US-09-292-072-25	Sequence 25, Appl
40	33	70.2	470	2	US-10-176-255-25	Sequence 25, Appl
41	33	70.2	471	1	US-07-817-920-8	Sequence 8, Appli
42	33	70.2	471	1	US-07-996-772A-11	Sequence 11, Appl
43	33	70.2	471	1	US-08-370-542-7	Sequence 7, Appli
44	33	70.2	471	1	US-08-117-006-8	Sequence 8, Appli
45	33	70.2	471	1	US-08-216-594-8	Sequence 8, Appli

ALIGNMENTS

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RESULT 1
US-09-359-503-9
; Sequence 9, Application US/09359503
; Patent No. 6251603
;  GENERAL INFORMATION:
;    APPLICANT:  Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
;    APPLICANT:  Knuth, alexander
;    TITLE OF INVENTION:  Method for Determining Status of A
;    TITLE OF INVENTION:  Cancerous Condition By Determining Antibodies          to NY
;    TITLE OF INVENTION:  a Patient Sample
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/359,503
;      FILING DATE:  July 23, 1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/165,546
;      FILING DATE:  October 2, 1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/062,422
;      FILING DATE:  April 17, 1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/937,263
;      FILING DATE:  September 15, 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/752,182
;      FILING DATE:  03-October-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 6251603man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3000
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 amino acids
;      TYPE:  amino acid
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;      TOPOLOGY:  linear
US-09-359-503-9

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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
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Db          7 TVSGNILTIR 16


RESULT 2
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; Sequence 13, Application US/09359503
; Patent No. 6251603
;  GENERAL INFORMATION:
;    APPLICANT:  Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
;    APPLICANT:  Knuth, alexander
;    TITLE OF INVENTION:  Method for Determining Status of A
;    TITLE OF INVENTION:  Cancerous Condition By Determining Antibodies          to NY-
;    TITLE OF INVENTION:  a Patient Sample
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/359,503
;      FILING DATE:  July 23, 1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/165,546
;      FILING DATE:  October 2, 1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/062,422
;      FILING DATE:  April 17, 1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/937,263
;      FILING DATE:  September 15, 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/752,182
;      FILING DATE:  03-October-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 6251603man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3000
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-09-359-503-13

  Query Match             100.0%;  Score 47;  DB 2;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
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Db          1 TVSGNILTIR 10


RESULT 3
US-09-165-546D-9
; Sequence 9, Application US/09165546D
; Patent No. 6723832
;  GENERAL INFORMATION:
;      APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
;                 Gure, Ali, Old, Lloyd, Ritter, Gerd
;      TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                          SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
;                          USES THEREOF
;      NUMBER OF SEQUENCES: 15
;      CORRESPONDENCE ADDRESS:
;           ADDRESSEE: FULBRIGHT & JAWORSKI LLP
;           STREET: 666 Fifth Avenue
;           CITY: New York City
;           STATE: New York
;           COUNTRY: USA
;           ZIP: 10158
;      COMPUTER READABLE FORM:
;           MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;           COMPUTER: IBM
;           OPERATING SYSTEM: PC-DOS
;           SOFTWARE: Word
;      CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/165,546D
;           FILING DATE: 02-Oct-1998
;           CLASSIFICATION: 530
;      PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 09/062,422
;           FILING DATE: April 17, 1998
;           APPLICATION NUMBER: 08/937,263
;           FILING DATE: September 15, 1997
;           APPLICATION NUMBER: US 08/725,182
;           FILING DATE: October 3, 1996
;      ATTORNEY/AGENT INFORMATION:
;           NAME: Hanson, No. 6723832man D.
;           REGISTRATION NUMBER: 30,946
;           REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;      TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (212) 318-3000
;           TELEFAX: (212) 318-3400
;   INFORMATION FOR SEQ ID NO: 9:
;      SEQUENCE CHARACTERISTICS:
;           LENGTH: 18 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;      SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-165-546D-9

  Query Match             100.0%;  Score 47;  DB 2;  Length 18;
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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
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Db          7 TVSGNILTIR 16


RESULT 4
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; Patent No. 6723832
;   GENERAL INFORMATION:
;      APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
;                 Gure, Ali, Old, Lloyd, Ritter, Gerd
;      TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                          SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
;                          USES THEREOF
;      NUMBER OF SEQUENCES: 15
;      CORRESPONDENCE ADDRESS:
;           ADDRESSEE: FULBRIGHT & JAWORSKI LLP
;           STREET: 666 Fifth Avenue
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;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10158
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: Word
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/165,546D
;             FILING DATE: 02-Oct-1998
;             CLASSIFICATION: 530
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: April 17, 1998
;             APPLICATION NUMBER: 08/937,263
;             FILING DATE: September 15, 1997
;             APPLICATION NUMBER: US 08/725,182
;             FILING DATE: October 3, 1996
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, No. 6723832man D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3000
;             TELEFAX: (212) 318-3400
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-165-546D-13

  Query Match             100.0%;  Score 47;  DB 2;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          1 TVSGNILTIR 10


RESULT 5
US-09-408-036B-8
; Sequence 8, Application US/09408036B
; Patent No. 6800730
; GENERAL INFORMATION:
;  APPLICANT: Tureci, Ozlem
;  APPLICANT:  Sahin, Ugur
;  APPLICANT:  Pfreundschuh, Michael
;  TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses T
;  FILE REFERENCE: LUD 5624
;  CURRENT APPLICATION NUMBER: US/09/408,036B
;  CURRENT FILING DATE:  1999-09-29
;  PRIOR APPLICATION NUMBER: 09/344,040
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: 09/165,546
;  PRIOR FILING DATE: 1998-10-02
;  NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 8
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-408-036B-8

  Query Match             100.0%;  Score 47;  DB 2;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          7 TVSGNILTIR 16


RESULT 6
US-09-408-036B-12
; Sequence 12, Application US/09408036B
; Patent No. 6800730
; GENERAL INFORMATION:
;  APPLICANT: Tureci, Ozlem
;  APPLICANT:  Sahin, Ugur
;  APPLICANT:  Pfreundschuh, Michael
;  TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses
;  FILE REFERENCE: LUD 5624
;  CURRENT APPLICATION NUMBER: US/09/408,036B
;  CURRENT FILING DATE:  1999-09-29
;  PRIOR APPLICATION NUMBER: 09/344,040
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: 09/165,546
;  PRIOR FILING DATE: 1998-10-02
;  NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 12
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-408-036B-12

  Query Match             100.0%;  Score 47;  DB 2;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          1 TVSGNILTIR 10


RESULT 7
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL-1 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180 amino acids
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;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-791-495-9

  Query Match             100.0%;  Score 47;  DB 1;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db        127 TVSGNILTIR 136


RESULT 8
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
;  GENERAL INFORMATION:
;    APPLICANT:  Chen, Yao-Tseng; Scanlan, Matthew;
;    APPLICANT:  Gure, Ali; Old, Lloyd J.; Jager, Elke;
;    APPLICANT:  Alexander, Knuth; Drijfhout, Jan W.
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULE
;    TITLE OF INVENTION:  ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
;    TITLE OF INVENTION:  ITSELF, AND USES THEREOF
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/937,263B
;      FILING DATE:  September 15, 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sinn, Eric, Patent Agent
;      REGISTRATION NUMBER:  40,177
;      REFERENCE/DOCKET NUMBER:  LUD 5466.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3000
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-937-263B-8

  Query Match             100.0%;  Score 47;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db        127 TVSGNILTIR 136


RESULT 9
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
;  GENERAL INFORMATION:
;    APPLICANT:  Stockert, Elisabeth; Jager, Elke;
;    APPLICANT:  Chen, Yao-tseng; Scanlan, Matthew;
;    APPLICANT:  Knuth, Alexander; Old, Lloyd J.
;    TITLE OF INVENTION:  Antibodies Which Bind to NY-ESO-1 Cancer
;    TITLE OF INVENTION:  Associated Proteins, Uses Thereof,
;    TITLE OF INVENTION:  Truncated Forms of NY-ESO-1, and HLA
;    TITLE OF INVENTION:  Binding Peptides Derived Therefrom
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/751,798
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/062,422
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 6525177man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3168
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-09-751-798-8

  Query Match             100.0%;  Score 47;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db        127 TVSGNILTIR 136


RESULT 10
US-09-392-714-25
; Sequence 25, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT: Gure, Ali O.
;  APPLICANT: Williamson, Barbara
;  APPLICANT: Chen, Yao-Tseng
;  APPLICANT: Old, Lloyd J.
;  TITLE OF INVENTION: Cancer Associated Antigens and Uses
;  TITLE OF INVENTION: Therefor
;  FILE REFERENCE: L0461/7062
;  CURRENT APPLICATION NUMBER: US/09/392,714A
;  CURRENT FILING DATE: 1999-09-09
;  EARLIER APPLICATION NUMBER: PCT/US98/14679
;  EARLIER FILING DATE: 1998-07-15
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
;   LENGTH: 180
;   TYPE: PRT
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;   ORGANISM: Homo sapiens
US-09-392-714-25

  Query Match             100.0%;  Score 47;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db        127 TVSGNILTIR 136


RESULT 11
US-09-165-546D-15
; Sequence 15, Application US/09165546D
; Patent No. 6723832
;   GENERAL INFORMATION:
;        APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
;                   Gure, Ali, Old, Lloyd, Ritter, Gerd
;        TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                            SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
;                            USES THEREOF
;        NUMBER OF SEQUENCES: 15
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FULBRIGHT & JAWORSKI LLP
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10158
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/165,546D
;             FILING DATE: 02-Oct-1998
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: April 17, 1998
;             APPLICATION NUMBER: 08/937,263
;             FILING DATE: September 15, 1997
;             APPLICATION NUMBER: US 08/725,182
;             FILING DATE: October 3, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, No. 6723832man D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3000
;             TELEFAX: (212) 318-3400
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 180 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15

  Query Match             100.0%;  Score 47;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db        127 TVSGNILTIR 136


RESULT 12
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-9

  Query Match             100.0%;  Score 47;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db        127 TVSGNILTIR 136


RESULT 13
US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT:  Old, Lloyd J.
;  APPLICANT:  Stockert, Elisabeth
;  APPLICANT:  Chen, Yao-Tseng
;  TITLE OF INVENTION: Colon Cancer Antigen Panel
;  FILE REFERENCE: L0461/7105(JRV)
;  CURRENT APPLICATION NUMBER: US/09/849,602
;  CURRENT FILING DATE:  2001-05-04
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-849-602-30

  Query Match             100.0%;  Score 47;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db        127 TVSGNILTIR 136


RESULT 14
US-09-344-040C-125
; Sequence 125, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
;  APPLICANT: Tureci, Ozlem
;  APPLICANT:  Sahin, Ugur
;  APPLICANT:  Pfreundschuh, Michael
;  APPLICANT:  Ramensee, Hans Georg
;  APPLICANT:  Stevanovic, Stefan
;  TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determi
;  TITLE OF INVENTION:  Expression of an SSX Gene, Peptides Derived From Said SSX Gene
;  TITLE OF INVENTION:  Gene, and Uses Thereof
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;  FILE REFERENCE: LUD 5556.1
;  CURRENT APPLICATION NUMBER: US/09/344,040C
;  CURRENT FILING DATE:  1999-06-25
;  PRIOR APPLICATION NUMBER: US 09/105,839
;  PRIOR FILING DATE: 1998-06-26
;  PRIOR APPLICATION NUMBER: US 08/851,130
;  PRIOR FILING DATE: 1997-05-05
;  NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 125
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-344-040C-125

  Query Match             89.4%;  Score 42;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTI 9
              |||||||||
Db          1 TVSGNILTI 9


RESULT 15
US-09-833-039A-125
; Sequence 125, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
;  APPLICANT: Tureci, Ozlem
;  APPLICANT:  Sahin, Ugur
;  APPLICANT:  Pfreundschuh, Michael
;  TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
;  FILE REFERENCE: LUD 5622.1
;  CURRENT APPLICATION NUMBER: US/09/833,039A
;  CURRENT FILING DATE:  2001-04-12
;  PRIOR APPLICATION NUMBER: US 09/409,455
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: US 09/344,040
;  PRIOR FILING DATE: 1999-06-26
;  PRIOR APPLICATION NUMBER: US 09/105,839
;  PRIOR FILING DATE: 1998-06-26
;  NUMBER OF SEQ ID NOS: 131
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 125
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
JS-09-833-039A-125

  Query Match             89.4%;  Score 42;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTI 9
              |||||||||
Db          1 TVSGNILTI 9


Search completed: March 13, 2006, 19:18:49
Job time : 18.5882 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:51:56 ; Search time 60.4706 Seconds
(without alignments)
69.096 Million cell updates/sec

Title: US-09-529-206E-15
Perfect score: 47
Sequence: 1 TVSGNILTIR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	47	100.0	14	5	US-10-182-506A-17	Sequence 17, Appl
2	47	100.0	15	5	US-10-182-506A-15	Sequence 15, Appl
3	47	100.0	15	5	US-10-182-506A-16	Sequence 16, Appl
4	47	100.0	18	4	US-10-751-088-9	Sequence 9, Appli
5	47	100.0	18	4	US-10-751-088-13	Sequence 13, Appl
6	47	100.0	18	4	US-10-851-884-8	Sequence 8, Appli
7	47	100.0	18	4	US-10-851-884-12	Sequence 12, Appl
8	47	100.0	18	5	US-10-182-506A-65	Sequence 65, Appl
9	47	100.0	20	4	US-10-164-121A-35	Sequence 35, Appl
10	47	100.0	20	4	US-10-164-078A-34	Sequence 34, Appl
11	47	100.0	20	5	US-10-182-506A-38	Sequence 38, Appl
12	47	100.0	20	5	US-10-941-150A-35	Sequence 35, Appl
13	47	100.0	25	5	US-10-491-891-83	Sequence 83, Appl
14	47	100.0	25	5	US-10-182-506A-7	Sequence 7, Appli
15	47	100.0	27	5	US-10-182-506A-6	Sequence 6, Appli
16	47	100.0	30	4	US-10-296-734-1414	Sequence 1414, Ap
17	47	100.0	54	4	US-10-447-161-140	Sequence 140, App
18	47	100.0	123	4	US-10-777-053-17	Sequence 17, Appl
19	47	100.0	123	4	US-10-837-217-17	Sequence 17, Appl
20	47	100.0	179	4	US-10-777-053-20	Sequence 20, Appl
21	47	100.0	179	4	US-10-837-217-20	Sequence 20, Appl
22	47	100.0	179	5	US-10-482-029-202	Sequence 202, App
23	47	100.0	180	3	US-09-751-798-8	Sequence 8, Appli
24	47	100.0	180	3	US-09-849-602-30	Sequence 30, Appl
25	47	100.0	180	4	US-10-023-182-8	Sequence 8, Appli
26	47	100.0	180	4	US-10-207-655-71	Sequence 71, Appl
27	47	100.0	180	4	US-10-026-066-3	Sequence 3, Appli
28	47	100.0	180	4	US-10-117-937-74	Sequence 74, Appl
29	47	100.0	180	4	US-10-295-027-386	Sequence 386, App
30	47	100.0	180	4	US-10-296-734-832	Sequence 832, App
31	47	100.0	180	4	US-10-188-832-139	Sequence 139, App
32	47	100.0	180	4	US-10-777-053-11	Sequence 11, Appl
33	47	100.0	180	4	US-10-751-088-15	Sequence 15, Appl
34	47	100.0	180	4	US-10-657-022-74	Sequence 74, Appl
35	47	100.0	180	4	US-10-837-217-11	Sequence 11, Appl
36	47	100.0	180	5	US-10-877-373-9	Sequence 9, Appli
37	47	100.0	180	5	US-10-723-860-1270	Sequence 1270, Ap
38	47	100.0	180	5	US-10-871-708-7	Sequence 7, Appli
39	47	100.0	180	5	US-10-895-523-3	Sequence 3, Appli
40	47	100.0	180	5	US-10-182-506A-3	Sequence 3, Appli
41	47	100.0	180	5	US-10-756-149-5024	Sequence 5024, Ap
42	47	100.0	180	6	US-11-067-064-74	Sequence 74, Appl
43	47	100.0	180	6	US-11-067-159-74	Sequence 74, Appl
44	47	100.0	397	3	US-09-821-883-27	Sequence 27, Appl
45	47	100.0	397	6	US-11-144-912-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-10-182-506A-17
; Sequence 17, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; TITLE OF INVENTION: ANTIGEN, NY ESO-1
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-17

Query Match 100.0%; Score 47; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNILTIR 10
||||||||||
Db 4 TVSGNILTIR 13

RESULT 2
US-10-182-506A-15
; Sequence 15, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; TITLE OF INVENTION: ANTIGEN, NY ESO-1
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A

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;  CURRENT FILING DATE:  2002-10-28
;  PRIOR APPLICATION NUMBER: PCT/US01/02765
;  PRIOR FILING DATE: 2001-01-26
;  PRIOR APPLICATION NUMBER: 60/179,004
;  PRIOR FILING DATE: 2000-01-28
;  PRIOR APPLICATION NUMBER: 60/237,107
;  PRIOR FILING DATE: 2000-09-29
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-182-506A-15

  Query Match             100.0%;  Score 47;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          6 TVSGNILTIR 15


RESULT 3
US-10-182-506A-16
; Sequence 16, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, R-F
;  APPLICANT:  Rosenberg, S A
;  APPLICANT:  Zeng, G
;  TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
;  TITLE OF INVENTION:  ANTIGEN, NY ESO-1
;  FILE REFERENCE: 217955
;  CURRENT APPLICATION NUMBER: US/10/182,506A
;  CURRENT FILING DATE:  2002-10-28
;  PRIOR APPLICATION NUMBER: PCT/US01/02765
;  PRIOR FILING DATE: 2001-01-26
;  PRIOR APPLICATION NUMBER: 60/179,004
;  PRIOR FILING DATE: 2000-01-28
;  PRIOR APPLICATION NUMBER: 60/237,107
;  PRIOR FILING DATE: 2000-09-29
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-182-506A-16

  Query Match             100.0%;  Score 47;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          5 TVSGNILTIR 14


RESULT 4
US-10-751-088-9
; Sequence 9, Application US/10751088
; Publication No. US20040158044A1
;   GENERAL INFORMATION:
;        APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
;                   Gure, Ali, Old, Lloyd, Ritter, Gerd
;        TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                            SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
;                            USES THEREOF
;        NUMBER OF SEQUENCES: 15
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FULBRIGHT & JAWORSKI LLP
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10158
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/751,088
;             FILING DATE: 02-Jan-2004
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/165,546D
;             FILING DATE: 02-Oct-1998
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: April 17, 1998
;             APPLICATION NUMBER: 08/937,263
;             FILING DATE: September 15, 1997
;             APPLICATION NUMBER: US 08/725,182
;             FILING DATE: October 3, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, Norman D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3000
;             TELEFAX: (212) 318-3400
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-751-088-9

  Query Match             100.0%;  Score 47;  DB 4;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 0.037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          7 TVSGNILTIR 16


RESULT 5
US-10-751-088-13
; Sequence 13, Application US/10751088
; Publication No. US20040158044A1
;   GENERAL INFORMATION:
;        APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
;                   Gure, Ali, Old, Lloyd, Ritter, Gerd
;        TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                            SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
;                            USES THEREOF
;        NUMBER OF SEQUENCES: 15
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FULBRIGHT & JAWORSKI LLP
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10158
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
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;            SOFTWARE: Word
;         CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/751,088
;            FILING DATE: 02-Jan-2004
;            CLASSIFICATION: 530
;         PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/165,546D
;            FILING DATE: 02-Oct-1998
;            APPLICATION NUMBER: 09/062,422
;            FILING DATE: April 17, 1998
;            APPLICATION NUMBER: 08/937,263
;            FILING DATE: September 15, 1997
;            APPLICATION NUMBER: US 08/725,182
;            FILING DATE: October 3, 1996
;         ATTORNEY/AGENT INFORMATION:
;            NAME: Hanson, Norman D.
;            REGISTRATION NUMBER: 30,946
;            REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;         TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 318-3000
;            TELEFAX: (212) 318-3400
;      INFORMATION FOR SEQ ID NO: 13:
;         SEQUENCE CHARACTERISTICS:
;            LENGTH: 18 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-751-088-13

  Query Match           100.0%;  Score 47;  DB 4;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 0.037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          1 TVSGNILTIR 10


RESULT 6
US-10-851-884-8
; Sequence 8, Application US/10851884
; Publication No. US20040214284A1
; GENERAL INFORMATION:
;  APPLICANT: Tureci, Ozlem
;  APPLICANT:  Sahin, Ugur
;  APPLICANT:  Pfreundschuh, Michael
;  TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses T
;  FILE REFERENCE: LUD 5624
;  CURRENT APPLICATION NUMBER: US/10/851,884
;  CURRENT FILING DATE:  2004-05-21
;  PRIOR APPLICATION NUMBER: US/09/408,036
;  PRIOR FILING DATE: 1999-09-29
;  PRIOR APPLICATION NUMBER: 09/344,040
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: 09/165,546
;  PRIOR FILING DATE: 1998-10-02
;  NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 8
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-851-884-8

  Query Match           100.0%;  Score 47;  DB 4;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 0.037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          7 TVSGNILTIR 16


RESULT 7
US-10-851-884-12
; Sequence 12, Application US/10851884
; Publication No. US20040214284A1
; GENERAL INFORMATION:
;  APPLICANT: Tureci, Ozlem
;  APPLICANT:  Sahin, Ugur
;  APPLICANT:  Pfreundschuh, Michael
;  TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses
;  FILE REFERENCE: LUD 5624
;  CURRENT APPLICATION NUMBER: US/10/851,884
;  CURRENT FILING DATE:  2004-05-21
;  PRIOR APPLICATION NUMBER: US/09/408,036
;  PRIOR FILING DATE: 1999-09-29
;  PRIOR APPLICATION NUMBER: 09/344,040
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: 09/165,546
;  PRIOR FILING DATE: 1998-10-02
;  NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 12
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-851-884-12

  Query Match           100.0%;  Score 47;  DB 4;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 0.037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          1 TVSGNILTIR 10


RESULT 8
US-10-182-506A-65
; Sequence 65, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, R-F
;  APPLICANT:  Rosenberg, S A
;  APPLICANT:  Zeng, G
;  TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
;  TITLE OF INVENTION:  ANTIGEN, NY ESO-1
;  FILE REFERENCE: 217955
;  CURRENT APPLICATION NUMBER: US/10/182,506A
;  CURRENT FILING DATE:  2002-10-28
;  PRIOR APPLICATION NUMBER: PCT/US01/02765
;  PRIOR FILING DATE: 2001-01-26
;  PRIOR APPLICATION NUMBER: 60/179,004
;  PRIOR FILING DATE: 2000-01-28
;  PRIOR APPLICATION NUMBER: 60/237,107
;  PRIOR FILING DATE: 2000-09-29
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-182-506A-65

  Query Match           100.0%;  Score 47;  DB 5;  Length 18;
  Best Local Similarity  100.0%;  Pred. No. 0.037;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db          7 TVSGNILTIR 16


RESULT 9
US-10-164-121A-35
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; Sequence 35, Application US/10164121A
; Publication No. US20030228308A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Boon, Thierry
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Traversari, Catra
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-Cw6 Molecules And Uses Thereo
; FILE REFERENCE: LUD-5771
; CURRENT APPLICATION NUMBER: US/10/164,121A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 35
; LENGTH: 20
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-121A-35

Query Match 100.0%; Score 47; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNILTIR 10
||||||||||
Db 9 TVSGNILTIR 18

RESULT 10
US-10-164-078A-34
; Sequence 34, Application US/10164078A
; Publication No. US20030228325A1
; GENERAL INFORMATION:
; APPLICANT: Bilsborough, Janine
; APPLICANT: Schultz, Erwin
; APPLICANT: Panichelli, Christophe
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B18 Molecules And Uses Thereo
; FILE REFERENCE: LUD-5756
; CURRENT APPLICATION NUMBER: US/10/164,078A
; CURRENT FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 34
; LENGTH: 20
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-078A-34

Query Match 100.0%; Score 47; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNILTIR 10
||||||||||
Db 9 TVSGNILTIR 18

RESULT 11
US-10-182-506A-38
; Sequence 38, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; TITLE OF INVENTION: ANTIGEN, NY ESO-1
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-38

Query Match 100.0%; Score 47; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNILTIR 10
||||||||||
Db 2 TVSGNILTIR 11

RESULT 12
US-10-941-150A-35
; Sequence 35, Application US/10941150A
; Publication No. US20050226881A1
; GENERAL INFORMATION:
; APPLICANT: VAN DER BRUGGEN, Pierre
; APPLICANT: BOON-FALLEUR, Thierry
; APPLICANT: BRECKPOT, Karine
; APPLICANT: THIELEMANS, Kris
; TITLE OF INVENTION: ISOLATED PEPTIDE WHICH BINDS TO HLA-CW*07 AND USES THEREOF
; FILE REFERENCE: LUD-5853-US (10411307)
; CURRENT APPLICATION NUMBER: US/10/941,150A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: US 60/504,874
; PRIOR FILING DATE: 2003-09-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from NY-ESO-1
US-10-941-150A-35

Query Match 100.0%; Score 47; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNILTIR 10
||||||||||
Db 9 TVSGNILTIR 18

RESULT 13
US-10-491-891-83
; Sequence 83, Application US/10491891
; Publication No. US20050059107A1
; GENERAL INFORMATION:
; APPLICANT: MAILLERE, BERNARD
; APPLICANT: CASTELLI, FLORENCE
; APPLICANT: BUHOT, CECILE
; APPLICANT: GEORGES, BERTRAND
; TITLE OF INVENTION: METHOD OF SELECTING HLA-DP4 LIGANDS AND THE APPLICATIONS THEREOF
; FILE REFERENCE: 251858US0XPCT
; CURRENT APPLICATION NUMBER: US/10/491,891
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: PCT/FR02/03555
; PRIOR FILING DATE: 2002-10-17

; PRIOR APPLICATION NUMBER: FR01/13352
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-491-891-83

Query Match 100.0%; Score 47; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNILTIR 10
||||||||||
Db 9 TVSGNILTIR 18

RESULT 14
US-10-182-506A-7
; Sequence 7, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; TITLE OF INVENTION: ANTIGEN, NY ESO-1
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-7

Query Match 100.0%; Score 47; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNILTIR 10
||||||||||
Db 15 TVSGNILTIR 24

RESULT 15
US-10-182-506A-6
; Sequence 6, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; TITLE OF INVENTION: ANTIGEN, NY ESO-1
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-6

Query Match 100.0%; Score 47; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNILTIR 10
||||||||||
Db 17 TVSGNILTIR 26

Search completed: March 13, 2006, 20:02:26
Job time : 61.4706 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:54:06 ; Search time 6.82353 Seconds
(without alignments)
40.793 Million cell updates/sec

Title: US-09-529-206E-15
Perfect score: 47
Sequence: 1 TVSGNILTIR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	47	100.0	20	7	US-11-032-498-36	Sequence 36, Appl
2	47	100.0	180	7	US-11-155-288-7	Sequence 7, Appli
3	47	100.0	240	7	US-11-021-441-28	Sequence 28, Appl
4	35	74.5	223	6	US-10-485-517-412	Sequence 412, App
5	34	72.3	305	7	US-11-098-686-10549	Sequence 10549, A
6	34	72.3	585	7	US-11-072-512-2739	Sequence 2739, Ap
7	33	70.2	313	7	US-11-190-188-7	Sequence 7, Appli
8	33	70.2	387	6	US-10-467-657-1556	Sequence 1556, Ap
9	33	70.2	426	6	US-10-873-528-34	Sequence 34, Appl
10	33	70.2	471	6	US-10-995-561-901	Sequence 901, App
11	33	70.2	517	6	US-10-641-678-47	Sequence 47, Appl
12	32	68.1	105	6	US-10-485-788A-711	Sequence 711, App
13	32	68.1	105	7	US-11-053-076-81	Sequence 81, Appl
14	32	68.1	123	6	US-10-467-657-1358	Sequence 1358, Ap
15	32	68.1	523	6	US-10-641-678-45	Sequence 45, Appl
16	31	66.0	92	6	US-10-485-788A-657	Sequence 657, App
17	31	66.0	92	7	US-11-053-076-19	Sequence 19, Appl
18	31	66.0	536	6	US-10-641-678-70	Sequence 70, Appl
19	31	66.0	1085	7	US-11-087-099-11646	Sequence 11646, A
20	31	66.0	2204	7	US-11-052-554A-174	Sequence 174, App
21	30	63.8	40	6	US-10-895-064-2370	Sequence 2370, Ap
22	30	63.8	40	7	US-11-129-741-2370	Sequence 2370, Ap
23	30	63.8	194	7	US-11-087-099-342	Sequence 342, App
24	30	63.8	201	5	US-09-810-501-21	Sequence 21, Appl
25	30	63.8	228	5	US-09-978-360A-516	Sequence 516, App
26	30	63.8	280	6	US-10-511-538-41	Sequence 41, Appl
27	30	63.8	319	7	US-11-098-686-11290	Sequence 11290, A
28	30	63.8	340	7	US-11-129-143-43	Sequence 43, Appl
29	30	63.8	350	7	US-11-165-024-3	Sequence 3, Appli
30	30	63.8	353	7	US-11-129-143-55	Sequence 55, Appl
31	30	63.8	359	6	US-10-055-877-159	Sequence 159, App
32	30	63.8	406	7	US-11-072-512-3928	Sequence 3928, Ap
33	30	63.8	482	7	US-11-087-099-390	Sequence 390, App
34	30	63.8	590	7	US-11-124-368A-183	Sequence 183, App
35	30	63.8	590	7	US-11-127-877-54	Sequence 54, Appl
36	30	63.8	668	6	US-10-467-657-5042	Sequence 5042, Ap
37	30	63.8	690	7	US-11-052-554A-232	Sequence 232, App
38	29.5	62.8	453	7	US-11-190-188-19	Sequence 19, Appl
39	29	61.7	23	7	US-11-152-366-233	Sequence 233, App
40	29	61.7	107	6	US-10-467-657-1054	Sequence 1054, Ap
41	29	61.7	125	6	US-10-467-657-2228	Sequence 2228, Ap
42	29	61.7	135	7	US-11-019-711-86	Sequence 86, Appl
43	29	61.7	155	7	US-11-096-568A-26866	Sequence 26866, A
44	29	61.7	168	7	US-11-087-099-6776	Sequence 6776, Ap
45	29	61.7	201	7	US-11-124-368A-265	Sequence 265, App

ALIGNMENTS

RESULT 1
US-11-032-498-36
; Sequence 36, Application US/11032498
; Publication No. US20050249743A1
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van der Bruggen, Pierre
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-A24 Molecule and Uses Thereof
; FILE REFERENCE: LUD 5881
; CURRENT APPLICATION NUMBER: US/11/032,498
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: US 60/535,751
; PRIOR FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: NY-ESO-1 peptide
US-11-032-498-36

Query Match 100.0%; Score 47; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNILTIR 10
||||||||||
Db 9 TVSGNILTIR 18

RESULT 2
US-11-155-288-7
; Sequence 7, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0

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; SEQ ID NO 7
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-155-288-7

  Query Match             100.0%;  Score 47;  DB 7;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.023;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db        127 TVSGNILTIR 136


RESULT 3
US-11-021-441-28
; Sequence 28, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
;  APPLICANT: DUBENSKY, Thomas W., Jr.
;  APPLICANT:  PORTNOY, Daniel A.
;  APPLICANT:  LUCKETT, William S., Jr.
;  APPLICANT:  COOK, David N.
;  TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
;  TITLE OF INVENTION:  EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 282172003900
;  CURRENT APPLICATION NUMBER: US/11/021,441
;  CURRENT FILING DATE:  2004-12-23
;  PRIOR APPLICATION NUMBER: US 60/616,750
;  PRIOR FILING DATE: 2004-10-06
;  PRIOR APPLICATION NUMBER: US 60/615,287
;  PRIOR FILING DATE: 2004-10-01
;  PRIOR APPLICATION NUMBER: US 60/599,377
;  PRIOR FILING DATE: 2004-08-05
;  PRIOR APPLICATION NUMBER: PCT/US2004/23881
;  PRIOR FILING DATE: 2004-07-23
;  PRIOR APPLICATION NUMBER: US 10/883,599
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: US 60/556,744
;  PRIOR FILING DATE: 2004-03-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion protein
US-11-021-441-28

  Query Match             100.0%;  Score 47;  DB 7;  Length 240;
  Best Local Similarity   100.0%;  Pred. No. 0.032;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||||||||
Db        187 TVSGNILTIR 196


RESULT 4
US-10-485-517-412
; Sequence 412, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
;  APPLICANT: University of Sheffield
;  APPLICANT:  Biosynexus Incorporated
;  APPLICANT:  Foster, Simon
;  APPLICANT:  Mond, James
;  TITLE OF INVENTION: Antigenic Polypeptides
;  FILE REFERENCE: P100629WO
;  CURRENT APPLICATION NUMBER: US/10/485,517
;  CURRENT FILING DATE:  2004-02-02
;  PRIOR APPLICATION NUMBER: GB 0118825.9
;  PRIOR FILING DATE: 2001-08-02
;  PRIOR APPLICATION NUMBER: GB 0200349.9
;  PRIOR FILING DATE: 2002-01-09
;  NUMBER OF SEQ ID NOS: 424
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 412
;   LENGTH: 223
;   TYPE: PRT
;   ORGANISM: Staphylococcus epidermidis
US-10-485-517-412

  Query Match             74.5%;  Score 35;  DB 6;  Length 223;
  Best Local Similarity   70.0%;  Pred. No. 8.1;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              || |||: ||
Db        132 TVGGNIMKIR 141


RESULT 5
US-11-098-686-10549
; Sequence 10549, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
;  APPLICANT: Kapur, Vivek and Gebhart, Connie J.
;  TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
;  TITLE OF INVENTION:  FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
;  FILE REFERENCE: 09531-128001
;  CURRENT APPLICATION NUMBER: US/11/098,686
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: PCT/US03/31318
;  PRIOR FILING DATE: 2003-10-01
;  PRIOR APPLICATION NUMBER: US 60/416,395
;  PRIOR FILING DATE: 2002-10-04
;  NUMBER OF SEQ ID NOS: 11433
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10549
;   LENGTH: 305
;   TYPE: PRT
;   ORGANISM: Lawsonia intracellularis
US-11-098-686-10549

  Query Match             72.3%;  Score 34;  DB 7;  Length 305;
  Best Local Similarity   77.8%;  Pred. No. 19;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 VSGNILTIR 10
              |||||| :|
Db         52 VSGNILPLR 60


RESULT 6
US-11-072-512-2739
; Sequence 2739, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
;  APPLICANT: ISOGAI, TAKAO
;  APPLICANT:  SUGIYAMA, TOMOYASU
;  APPLICANT:  OTSUKI, TETSUJI
;  APPLICANT:  WAKAMATSU, AI
;  APPLICANT:  SATO, HIROYUKI
;  APPLICANT:  ISHII, SHIZUKO
;  APPLICANT:  YAMAMOTO, JUN-ICHI
;  APPLICANT:  ISONO, YUUKO
;  APPLICANT:  HIO, YURI
;  APPLICANT:  OTSUKA, KAORU
;  APPLICANT:  NAGAI, KEIICHI
;  APPLICANT:  IRIE, RYOTARO
;  APPLICANT:  TAMECHIKA, ICHIRO
;  APPLICANT:  SEKI, NAOHIKO
```

```
;  APPLICANT:  YOSHIKAWA, TSUTOMU
;  APPLICANT:  OTSUKA, MOTOYUKI
;  APPLICANT:  NAGAHARI, KENJI
;  APPLICANT:  MASUHO, YASUHIKO
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: 084335-0191
;  CURRENT APPLICATION NUMBER: US/11/072,512
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: US 60/350,978
;  PRIOR FILING DATE: 2002-01-25
;  PRIOR APPLICATION NUMBER: JP 2001-379298
;  PRIOR FILING DATE: 2001-11-05
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2739
;   LENGTH: 585
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-072-512-2739

  Query Match             72.3%;  Score 34;  DB 7;  Length 585;
  Best Local Similarity   77.8%;  Pred. No. 40;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTI 9
              | ||||||:
Db        387 TPSGNILTL 395


RESULT 7
US-11-190-188-7
; Sequence 7, Application US/11190188
; Publication No. US20060035331A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  LAL, Preeti
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  PATTERSON, Chandra
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  SHIH, Leo L.
;  APPLICANT:  TRIBOULEY, Catherine
;  APPLICANT:  LU, Dyung Aina M.
;  APPLICANT:  YUE, Henry
;  APPLICANT:  KHAN, Farrah A.
;  APPLICANT:  POLICKY, Jennifer L.
;  APPLICANT:  AU-YOUNG, Janice
;  APPLICANT:  YANG, Junming
;  APPLICANT:  HARLAND, Lee
;  APPLICANT:  WALSH, Roderick T.
;  APPLICANT:  LO, Terence P.
;  APPLICANT:  BOROWSKY, Mark L.
;  TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: PI-0044 PCT
;  CURRENT APPLICATION NUMBER: US/11/190,188
;  CURRENT FILING DATE:  2005-07-27
;  PRIOR APPLICATION NUMBER: US/10/220,382
;  PRIOR FILING DATE: 2001-03-01
;  PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
;  PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PERL Program
; SEQ ID NO 7
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 3082743CD1
US-11-190-188-7

  Query Match             70.2%;  Score 33;  DB 7;  Length 313;
  Best Local Similarity   77.8%;  Pred. No. 31;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTI 9
              |:||||| |
Db         38 TLSGNILII 46


RESULT 8
US-10-467-657-1556
; Sequence 1556, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1556
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1556

  Query Match             70.2%;  Score 33;  DB 6;  Length 387;
  Best Local Similarity   77.8%;  Pred. No. 39;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 VSGNILTIR 10
              |||| || |
Db         77 VSGNFLTAR 85


RESULT 9
US-10-873-528-34
; Sequence 34, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
;  APPLICANT: Microbial Technics Limited
;  APPLICANT:  Gilbert, Christophe FG
;  APPLICANT:  Hansbro, Philip M
;  TITLE OF INVENTION: Proteins
;  FILE REFERENCE: PWC/P21129WO
;  CURRENT APPLICATION NUMBER: US/10/873,528
;  CURRENT FILING DATE:  2004-06-23
;  PRIOR APPLICATION NUMBER: US/09/769,787
;  PRIOR FILING DATE: 2001-01-26
;  PRIOR APPLICATION NUMBER: GB 9816337.1
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: US 60/125164
;  PRIOR FILING DATE: 1999-03-19
;  NUMBER OF SEQ ID NOS: 388
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
;   LENGTH: 426
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae
US-10-873-528-34

  Query Match             70.2%;  Score 33;  DB 6;  Length 426;
  Best Local Similarity   66.7%;  Pred. No. 44;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTI 9
              :|:|||:||
Db         45 SVAGNIITI 53
```

```
RESULT 10
US-10-995-561-901
; Sequence 901, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 901
;   LENGTH: 471
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-995-561-901

  Query Match             70.2%;  Score 33;  DB 6;  Length 471;
  Best Local Similarity   66.7%;  Pred. No. 50;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTI 9
              |::|||| |
Db         88 TIAGNILVI 96


RESULT 11
US-10-641-678-47
; Sequence 47, Application US/10641678
; Publication No. US20050277172A1
; GENERAL INFORMATION:
;  APPLICANT: Day, Anthony, G.
;  APPLICANT:  Goedegebuur, Frits
;  APPLICANT:  Gualfetti, Peter
;  APPLICANT:  Mitchinson, Colin
;  APPLICANT:  Neefe, Paulien
;  APPLICANT:  Sandgren, Mats
;  APPLICANT:  Shaw, Andrew
;  APPLICANT:  Stahlberg, Jerry
;  TITLE OF INVENTION: Novel Variant Hypocrea jecorina CBH1
;  TITLE OF INVENTION:  Cellulases
;  FILE REFERENCE: GC772-3
;  CURRENT APPLICATION NUMBER: US/10/641,678
;  CURRENT FILING DATE:  2003-08-15
;  PRIOR APPLICATION NUMBER: US 60/458,853
;  PRIOR FILING DATE: 2003-03-27
;  PRIOR APPLICATION NUMBER: US 60/458,696
;  PRIOR FILING DATE: 2003-03-27
;  PRIOR APPLICATION NUMBER: US 60/456,368
;  PRIOR FILING DATE: 2003-03-21
;  PRIOR APPLICATION NUMBER: US 60/404,063
;  PRIOR FILING DATE: 2002-08-16
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47
;   LENGTH: 517
;   TYPE: PRT
;   ORGANISM: Irpex lacteus
US-10-641-678-47

  Query Match             70.2%;  Score 33;  DB 6;  Length 517;
  Best Local Similarity   60.0%;  Pred. No. 56;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              | ||| ||::
Db        102 TTSGNALTLK 111


RESULT 12
US-10-485-788A-711
; Sequence 711, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
;  APPLICANT: Lu, Peter S.
;  APPLICANT:  Rabinowitz, Joshua D.
;  APPLICANT:  Schweizer, Johannes
;  APPLICANT:  Carrick, Deanna Marie
;  APPLICANT:  Arbor Vita Corporation
;  TITLE OF INVENTION: Molecular Interactions in Cells
;  FILE REFERENCE: 20054-003320US
;  CURRENT APPLICATION NUMBER: US/10/485,788A
;  CURRENT FILING DATE:  2004-02-03
;  PRIOR APPLICATION NUMBER: US 60/309,841
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: US 60/360,061
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: WO PCT/US02/24655
;  PRIOR FILING DATE: 2002-08-02
;  NUMBER OF SEQ ID NOS: 841
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 711
;   LENGTH: 105
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-485-788A-711

  Query Match             68.1%;  Score 32;  DB 6;  Length 105;
  Best Local Similarity   80.0%;  Pred. No. 14;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TVSGNILTIR 10
              ||||| | ||
Db         19 TVSGNGLGIR 28


RESULT 13
US-11-053-076-81
; Sequence 81, Application US/11053076
; Publication No. US20050255460A1
; GENERAL INFORMATION:
;  APPLICANT: Lu, Peter S.
;  APPLICANT:  Schweizer, Johannes
;  APPLICANT:  Somoza Diaz-Sarmiento, Chamorro
;  APPLICANT:  Belmares, Michael P.
;  TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
;  FILE REFERENCE: VITA-008CIP
;  CURRENT APPLICATION NUMBER: US/11/053,076
;  CURRENT FILING DATE:  2005-02-07
;  PRIOR APPLICATION NUMBER: PCT/US03/28508
;  PRIOR FILING DATE: 2003-09-09
;  PRIOR APPLICATION NUMBER: 10/630,590
;  PRIOR FILING DATE: 2003-07-29
;  PRIOR APPLICATION NUMBER: 60/490,094
;  PRIOR FILING DATE: 2003-07-25
;  PRIOR APPLICATION NUMBER: 60/450,464
;  PRIOR FILING DATE: 2003-02-27
;  PRIOR APPLICATION NUMBER: 60/409,298
;  PRIOR FILING DATE: 2002-09-09
;  PRIOR APPLICATION NUMBER: 10/630,590
;  PRIOR FILING DATE: 2003-07-29
;  PRIOR APPLICATION NUMBER: PCT/US02/24655
;  PRIOR FILING DATE: 2002-08-02
;  PRIOR APPLICATION NUMBER: 60/309,841
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: 60/360,061
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: 10/080,273
;  PRIOR FILING DATE: 2002-02-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 330
;  SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 81
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-053-076-81

Query Match 68.1%; Score 32; DB 7; Length 105;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 TVSGNILTIR 10
              ||||| | ||
Db         19 TVSGNGLGIR 28
```

RESULT 14
US-10-467-657-1358
; Sequence 1358, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1358
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1358

Query Match 68.1%; Score 32; DB 6; Length 123;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TVSGNIL 7
              |||||:|
Db         95 TVSGNVL 101
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RESULT 15
US-10-641-678-45
; Sequence 45, Application US/10641678
; Publication No. US20050277172A1
; GENERAL INFORMATION:
; APPLICANT: Day, Anthony, G.
; APPLICANT: Goedegebuur, Frits
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Neefe, Paulien
; APPLICANT: Sandgren, Mats
; APPLICANT: Shaw, Andrew
; APPLICANT: Stahlberg, Jerry
; TITLE OF INVENTION: Novel Variant Hypocrea jecorina CBH1
; TITLE OF INVENTION: Cellulases
; FILE REFERENCE: GC772-3
; CURRENT APPLICATION NUMBER: US/10/641,678
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/458,853
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/458,696
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/456,368
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US 60/404,063
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Irpex lacteus
US-10-641-678-45

Query Match 68.1%; Score 32; DB 6; Length 523;
Best Local Similarity 60.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 TVSGNILTIR 10
              | ||| ||::
Db        102 TTSGNALTLQ 111
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Search completed: March 13, 2006, 20:03:29
Job time : 6.82353 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 18:52:59 ; Search time 75.2941 Seconds
(without alignments)
58.355 Million cell updates/sec

Title: US-09-529-206E-25
Perfect score: 55
Sequence: 1 ASGPGGGAPR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	100.0	10	2	AAY06015	Aay06015 Human can
2	55	100.0	10	2	AAY05969	Aay05969 Human can
3	55	100.0	10	4	AAB31331	Aab31331 Exemplary
4	55	100.0	10	4	AAE07734	Aae07734 Human MHC
5	55	100.0	10	5	ABG66802	Abg66802 Tumour an
6	55	100.0	10	8	ADG89596	Adg89596 Class I H
7	55	100.0	10	9	ADX08546	Adx08546 Class I H
8	55	100.0	11	2	AAY06068	Aay06068 Human can
9	55	100.0	11	2	AAY06066	Aay06066 Human can
10	55	100.0	12	2	AAY06065	Aay06065 Human can
11	55	100.0	13	2	AAY06064	Aay06064 Human can
12	55	100.0	14	2	AAY05986	Aay05986 Human can
13	55	100.0	15	2	AAY05978	Aay05978 Human can
14	55	100.0	20	2	AAY05979	Aay05979 Human can
15	55	100.0	30	5	AAU85105	Aau85105 Human NYN
16	55	100.0	179	8	ADK68648	Adk68648 Epitope 1
17	55	100.0	180	2	AAW62584	Aaw62584 Cancer as
18	55	100.0	180	2	AAW69665	Aaw69665 Human NY-
19	55	100.0	180	2	AAY05965	Aay05965 Human can
20	55	100.0	180	3	AAY52430	Aay52430 Human tum
21	55	100.0	180	3	AAY70862	Aay70862 Human tum
22	55	100.0	180	3	AAB03154	Aab03154 Human oes
23	55	100.0	180	4	AAB69946	Aab69946 Human NY-
24	55	100.0	180	4	AAG67164	Aag67164 Amino aci
25	55	100.0	180	4	AAU01535	Aau01535 Human NY-
26	55	100.0	180	4	AAE07714	Aae07714 Human NY
27	55	100.0	180	5	AAU84818	Aau84818 Human NYN
28	55	100.0	180	5	AAU11543	Aau11543 Human tum
29	55	100.0	180	6	ABR58672	Abr58672 Human can
30	55	100.0	180	6	ABR48210	Abr48210 Human bla
31	55	100.0	180	6	ABU56508	Abu56508 Lung canc
32	55	100.0	180	6	ABU56694	Abu56694 Lung canc
33	55	100.0	180	6	ABP74198	Abp74198 Human NY-
34	55	100.0	180	6	ABU64816	Abu64816 Human NY-
35	55	100.0	180	6	ABR83438	Abr83438 Human NY-
36	55	100.0	180	7	ADC09576	Adc09576 NY-ESO-1
37	55	100.0	180	7	ADD35564	Add35564 Human NY-
38	55	100.0	180	7	ADD35568	Add35568 Human NY-
39	55	100.0	180	7	ADD25510	Add25510 Binding d
40	55	100.0	180	7	ADN39068	Adn39068 Cancer/an
41	55	100.0	180	8	ADJ54139	Adj54139 Human NY-
42	55	100.0	180	8	ADM72815	Adm72815 Human NY-
43	55	100.0	180	8	ADM73418	Adm73418 CAG-3 pro
44	55	100.0	180	8	ADM73417	Adm73417 Human NY-
45	55	100.0	180	8	ADQ18451	Adq18451 Human sof

ALIGNMENTS

RESULT 1
AAY06015
ID AAY06015 standard; peptide; 10 AA.
XX
AC AAY06015;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Example 10; Page 42; 88pp; English.
XX
CC This peptide was identified as an HLA peptide motif following a screen
CC for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see
CC AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified. The present
CC peptide (ranked 28) corresponds to amino acid residues 53-62 of CAG-1
CC ORF1 (see AAY05965). CAG-1 is a new and potent tumour antigen capable of
CC eliciting an antigen specific immune response by T cells. Cancer peptides
CC (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their
CC variants, are useful as cancer vaccines. A claimed method of preventing
CC or inhibiting cancer involves administering a cancer peptide, with or

CC without an HLA molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma, lymphoma,
CC sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
CC cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
CC prostate, ovarian, pancreatic and thyroid cancers
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
||||||||||
Db 1 ASGPGGGAPR 10

RESULT 2
AAY05969
ID AAY05969 standard; peptide; 10 AA.
XX
AC AAY05969;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
DR N-PSDB; AAX58600.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Claim 11; Page 64; 88pp; English.
XX
CC The present sequence represents a cancer peptide that is based on amino
CC acid residues 55-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965),
CC a new and potent tumour antigen capable of eliciting an antigen specific
CC immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-
CC 3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-
CC 87), are useful as cancer vaccines that protect against cancer. The
CC invention provides: vectors and host cells (also useful as vaccines); a
CC method of diagnosis of cancer or precancer; a transgenic animal;
CC antisense oligonucleotides that inhibit expression of the cancer peptide
CC or tumour antigen; antibodies reacting with a CAG-3 cancer peptide,
CC useful in diagnostic and detection assays; and methods for preventing or
CC inhibiting cancer by administering a cancer peptide, with or without an
CC HLA molecule. The cancer peptides form part of, or are derived from,
CC cancers such as primary or metastatic melanoma, thymoma, lymphoma,
CC sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
CC cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
CC prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by
CC inducing cancer-specific T cells in vitro for subsequent return to a
CC patient
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
||||||||||
Db 1 ASGPGGGAPR 10

RESULT 3
AAB31331
ID AAB31331 standard; peptide; 10 AA.
XX
AC AAB31331;
XX
DT 20-APR-2001 (first entry)
XX
DE Exemplary antigen characteristic of tumours and derived from NY-ESO-1.
XX
KW MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer;
KW MAGE-A1 HLA class II-binding protein; vaccine.
XX
OS Homo sapiens.
XX
PN WO200078806-A1.
XX
PD 28-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016287.
XX
PR 18-JUN-1999; 99US-00336091.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Van Snick J, Lethe B, Chaux P, Boon-Falleur T, Van Der Bruggen P;
XX
DR WPI; 2001-102698/11.
XX
PT Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and
PT are presented to the class II molecules, useful for inducing immune
PT response and treating cancers characterized by expression of MAGE-A1.
XX
PS Disclosure; Page 32; 78pp; English.
XX
CC AAB31302-59 represent exemplary antigens which are characteristic of
CC tumours. They can be used to enhance the immune response of vaccines
CC comprising peptides derived from human MAGE-A1 HLA (human leukocyte
CC antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA
CC binding protein stimulate the activity and proliferation of CD4+ T
CC lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic
CC agent for diagnosing a disorder characterized by expression of MAGE-A1.
CC The protein is used for treating a disorder characterized by expression
CC of MAGE-A1 such as cancers e.g. melanomal, squamous cell carcinomas,
CC colorectal carcinomas, osteosarcomas, and lymphocytic leukemias. Peptides
CC derived from the MAGE-A1 HLA binding protein are useful in the production
CC of anti-tumour vaccines
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
||||||||||
Db 1 ASGPGGGAPR 10

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RESULT 4
AAE07734
ID   AAE07734 standard; peptide; 10 AA.
XX
AC   AAE07734;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human MHC class I restricted NY ESO-1 cancer peptide #2.
XX
KW   Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW   class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW   NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW   tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW   immunotherapy.
XX
OS   Homo sapiens.
XX
PN   WO200155393-A2.
XX
PD   02-AUG-2001.
XX
PF   26-JAN-2001; 2001WO-US002765.
XX
PR   28-JAN-2000; 2000US-0179004P.
PR   29-SEP-2000; 2000US-0237107P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang R,  Rosenberg SA,  Zeng G;
XX
DR   WPI; 2001-496851/54.
XX
PT   New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT   useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT   protection from metastasis.
XX
PS   Claim 16; Page 84; 134pp; English.
XX
CC   The invention relates to the identification and isolation of major
CC   histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC   epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC   from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC   antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC   restricted. The products of the gene are promising candidates for
CC   immunotherapeutic strategies for the prevention, treatment and diagnosis
CC   of patients with cancer. The cancer epitopes are useful as immunogen and
CC   vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC   lymphocytes resulting in protection of the recipient from development of
CC   cancer and protection from metastasis, or by inhibiting the growth of
CC   cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC   useful as diagnostic agent to detect the presence of cancer, to enhance
CC   the generation of antibody and/or CD8+ T cell responses against any given
CC   target antigen and/or hapten and to induce tumour-specific humoral-
CC   mediated immunity against cancer. The present sequence is MHC class I
CC   restricted human NY ESO-1 cancer peptide
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 55;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.6;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db          1 ASGPGGGAPR 10


RESULT 5
ABG66802
ID   ABG66802 standard; peptide; 10 AA.
XX
AC   ABG66802;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Tumour antigen NY-ESO-1/CAG3 ORF1, HLA-A31 epitope.
XX
KW   Beta-2 microglobulin; beta-2m; cytotoxic T lymphocyte; CTL; HLA;
KW   human leukocyte antigen; fusion protein; epitope; cytostatic; tumour;
KW   gastrointestinal tumour; colorectal cancer; gastro-oesophageal cancer;
KW   liver cancer; biliary tract cancer; pancreatic cancer; vaccine;
KW   prostatic cancer; testicular cancer; lung cancer; breast cancer;
KW   malignant melanoma; mesothelioma; brain tumour; ovarian cancer;
KW   uterine cancer; cervical cancer; head and neck cancer; bladder cancer;
KW   Kaposi's sarcoma; renal carcinoma; leukaemia; lymphoma;
KW   acquired immunodeficiency syndrome; AIDS-related lymphoma.
XX
OS   Homo sapiens.
XX
PN   WO200236146-A2.
XX
PD   10-MAY-2002.
XX
PF   01-NOV-2001; 2001WO-GB004844.
XX
PR   02-NOV-2000; 2000GB-00026812.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
XX
PI   Tafuro S,  Meier U,  Mcmichael AJ,  Bell JI,  Layton G,  Hunter M;
XX
DR   WPI; 2002-508108/54.
XX
PT   New polynucleotide capable of expressing an epitope-beta2m fusion protein
PT   useful for generating cytotoxic T lymphocyte responses against a tumor
PT   and in restoring antigen presentation in the tumor of a host.
XX
PS   Disclosure; Page 25; 46pp; English.
XX
CC   The invention relates to a new polynucleotide capable of expressing an
CC   epitope-beta_2m fusion protein useful for generating cytotoxic T
CC   lymphocyte (CTL) responses against a tumour or in restoring antigen
CC   presentation in the tumour of a host. Also included are a polynucleotide
CC   capable of expressing an epitope-beta_2m fusion protein in combination
CC   with a vaccination agent that stimulates a CTL response against the
CC   epitope of the fusion protein for simultaneous, separate or sequential
CC   use in the treatment of cancer and a method of treating a tumour by
CC   administering a capable of expressing an epitope-beta_2m fusion protein,
CC   and optionally a vaccination agent that stimulates a CTL response against
CC   the epitope of the fusion protein. The polynucleotide is useful for
CC   generating CTL responses against tumours, for restoring antigen
CC   presentation in the tumour, and subsequently for treating cancers, such
CC   as gastrointestinal tumour, prostatic, testicular, lung or breast cancer,
CC   malignant melanoma, mesothelioma, brain tumour, ovarian cancer, uterine
CC   cancer including cervical cancer, cancer of the head and neck, bladder
CC   cancer, Kaposi's sarcoma, AIDS (acquired immunodeficiency syndrome)-
CC   related Kaposi's sarcoma, sarcomas, osteosarcoma, renal carcinoma, and
CC   haematopoietic malignant tumours such as leukaemia and lymphoma. The
CC   epitope is an HLA (human leukocyte antigen) peptide derived from a viral
CC   or tumour antigen. The present sequence is a tumour HLA epitope used in
CC   the fusion proteins of the invention
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 55;  DB 5;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.6;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db          1 ASGPGGGAPR 10


RESULT 6
```

ADG89596
ID ADG89596 standard; peptide; 10 AA.
XX
AC ADG89596;
XX
DT 11-MAR-2004 (first entry)
XX
DE Class I HLA-restricted testis cancer antigen #31.
XX
KW metastatic cancer cell differentiation; mutated fibronectin;
KW metastatic cancer; class I HLA-restricted; testis; cancer antigen.
XX
OS Unidentified.
XX
PN WO2003100027-A2.
XX
PD 04-DEC-2003.
XX
PF 28-MAY-2003; 2003WO-US016736.
XX
PR 28-MAY-2002; 2002US-0383530P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Wang R;
XX
DR WPI; 2004-035134/03.
XX
PT Identifying a cell that differentiates into a metastatic cancer cell,
PT useful for preventing metastatic cancer, comprises identifying a mutated
PT fibronectin in the cell.
XX
PS Disclosure; SEQ ID NO 39; 137pp; English.
XX
CC The invention comprises a method for identifying a cell that will
CC differentiate into a metastatic cancer cell, the method involves
CC identifying a mutated fibronectin in the cell. The method of the
CC invention is useful for preventing metastatic cancer. The present amino
CC acid sequence represents a Class I HLA-restricted testis cancer antigen.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
||||||||||
Db 1 ASGPGGGAPR 10

RESULT 7
ADX08546
ID ADX08546 standard; peptide; 10 AA.
XX
AC ADX08546;
XX
DT 21-APR-2005 (first entry)
XX
DE Class I HLA-restricted cancer/testis antigen peptide #31.
XX
KW vaccine; infection; viral infections; virucide; bacterial infection;
KW antibacterial; yeast infection; fungicide; fungal infection;
KW protozoal infection; protozoacide; cancer; cytostatic; melanoma;
KW lung tumor; colon tumor; breast tumor; leukemia; autoimmune disease;
KW multiple sclerosis; neuroprotective; rheumatoid arthritis; antiarthritic;
KW antirheumatic; systemic lupus erythematosus; antiinflammatory;
KW dermatological; immunosuppressive.
XX
OS Unidentified.
XX
PN WO2005011730-A1.
XX
PD 10-FEB-2005.
XX
PF 30-JUL-2004; 2004WO-GB003285.
XX
PR 01-AUG-2003; 2003GB-00018096.
XX
PA (UNLO) QUEEN MARY & WESTFIELD COLLEGE.
XX
PI Wang P, Li S;
XX
DR WPI; 2005-152360/16.
XX
PT New vaccine composition comprises inverted microsomes from animal cells
PT with an externally disposed peptide antigen and a protein of the Major
PT Histocompatibility Complex (MHC), useful for treating or preventing, e.g.
PT cancer.
XX
PS Disclosure; Page 48; 83pp; English.
XX
CC The invention comprises a vaccine composition that consists of isolated
CC inverted microsomes from an animal cell (or its membrane fragments), in
CC association with an externally disposed peptide antigen and a protein of
CC the MHC. The vaccine composition of the invention is useful for the
CC prophylaxis or treatment of: infection (e.g. viral, bacterial, yeast,
CC fungal or protozoal), cancer (e.g. melanoma, lung adenocarcinoma, colon
CC cancer, breast cancer or leukemia), autoimmune disease (e.g. multiple
CC sclerosis, rheumatoid arthritis or systemic lupus erythematosus). The
CC present amino acid sequence represents a class I HLA-restricted cancer
CC antigen which was found to be expressed by normal spermatocytes and/or
CC spermatogonia of testis.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
||||||||||
Db 1 ASGPGGGAPR 10

RESULT 8
AAY06068
ID AAY06068 standard; peptide; 11 AA.
XX
AC AAY06068;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 peptide.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;

XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Example 11; Page 50; 88pp; English.
XX
CC This peptide corresponds to amino acid residues 53-63 of human NY ESO-
CC 1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is
CC capable of eliciting an antigen specific immune response by T cells.
CC Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3
CC and their variants, are useful as cancer vaccines. A claimed method of
CC preventing or inhibiting cancer involves administering a cancer peptide,
CC with or without an HLA molecule. The cancer peptides form part of, or are
CC derived from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC as breast, prostate, ovarian, pancreatic and thyroid cancers
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 55; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
||||||||||
Db 1 ASGPGGGAPR 10

RESULT 9
AAY06066
ID AAY06066 standard; peptide; 11 AA.
XX
AC AAY06066;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 peptide.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Example 11; Page 50; 88pp; English.
XX
CC This peptide corresponds to amino acid residues 52-62 of human NY ESO-
CC 1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is
CC capable of eliciting an antigen specific immune response by T cells.
CC Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3
CC and their variants, are useful as cancer vaccines. A claimed method of
CC preventing or inhibiting cancer involves administering a cancer peptide,
CC with or without an HLA molecule. The cancer peptides form part of, or are
CC derived from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC as breast, prostate, ovarian, pancreatic and thyroid cancers
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 55; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
||||||||||
Db 2 ASGPGGGAPR 11

RESULT 10
AAY06065
ID AAY06065 standard; peptide; 12 AA.
XX
AC AAY06065;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 peptide.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Example 11; Page 50; 88pp; English.
XX
CC This peptide corresponds to amino acid residues 51-62 of human NY ESO-
CC 1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is
CC capable of eliciting an antigen specific immune response by T cells.
CC Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3
CC and their variants, are useful as cancer vaccines. A claimed method of
CC preventing or inhibiting cancer involves administering a cancer peptide,
CC with or without an HLA molecule. The cancer peptides form part of, or are
CC derived from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC as breast, prostate, ovarian, pancreatic and thyroid cancers
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 55; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ASGPGGGAPR 10
              ||||||||||
Db          3 ASGPGGGAPR 12


RESULT 11
AAY06064
ID   AAY06064 standard; peptide; 13 AA.
XX
AC   AAY06064;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 peptide.
XX
KW   NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW   leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW   metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW   uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW   cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW   liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW   vaccine; cytotoxic T lymphocyte; CTL.
XX
OS   Homo sapiens.
XX
PN   WO9918206-A2.
XX
PD   15-APR-1999.
XX
PF   21-SEP-1998;   98WO-US019609.
XX
PR   08-OCT-1997;   97US-0061428P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang RF,  Rosenberg SA;
XX
DR   WPI; 1999-277270/23.
XX
PT   Cancer antigen NY ESO1/CAG-3.
XX
PS   Example 11; Page 50; 88pp; English.
XX
CC   This peptide corresponds to amino acid residues 50-62 of human NY ESO-
CC   1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is
CC   capable of eliciting an antigen specific immune response by T cells.
CC   Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3
CC   and their variants, are useful as cancer vaccines. A claimed method of
CC   preventing or inhibiting cancer involves administering a cancer peptide,
CC   with or without an HLA molecule. The cancer peptides form part of, or are
CC   derived from, cancers such as primary or metastatic melanoma, thymoma,
CC   lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC   cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC   as breast, prostate, ovarian, pancreatic and thyroid cancers
XX
SQ   Sequence 13 AA;

  Query Match             100.0%;  Score 55;  DB 2;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0.76;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db          4 ASGPGGGAPR 13


RESULT 12
AAY05986
ID   AAY05986 standard; peptide; 14 AA.
XX
AC   AAY05986;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
KW   NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW   leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW   metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW   uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW   cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW   liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW   vaccine.
XX
OS   Homo sapiens.
XX
PN   WO9918206-A2.
XX
PD   15-APR-1999.
XX
PF   21-SEP-1998;   98WO-US019609.
XX
PR   08-OCT-1997;   97US-0061428P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang RF,  Rosenberg SA;
XX
DR   WPI; 1999-277270/23.
XX
PT   Cancer antigen NY ESO1/CAG-3.
XX
PS   Claim 25; Page 50; 88pp; English.
XX
CC   The present sequence represents a cancer peptide that corresponds to
CC   amino acid residues 49-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
CC   AAY05965), a new and potent tumour antigen capable of eliciting an
CC   antigen specific immune response by T cells. Cancer peptides derived from
CC   CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
CC   variants (see AAY05967-87), are useful as cancer vaccines that protect
CC   against cancer. The invention provides: vectors and host cells (also
CC   useful as vaccines); a method of diagnosis of cancer or precancer; a
CC   transgenic animal; antisense oligonucleotides that inhibit expression of
CC   the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
CC   cancer peptide, useful in diagnostic and detection assays; and methods
CC   for preventing or inhibiting cancer by administering a cancer peptide,
CC   with or without an HLA molecule. The cancer peptides form part of, or are
CC   derived from, cancers such as primary or metastatic melanoma, thymoma,
CC   lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC   cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC   as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
CC   treated by inducing cancer-specific T cells in vitro for subsequent
CC   return to a patient
XX
SQ   Sequence 14 AA;

  Query Match             100.0%;  Score 55;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0.81;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db          5 ASGPGGGAPR 14


RESULT 13
AAY05978
ID   AAY05978 standard; peptide; 15 AA.
XX
AC   AAY05978;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
```

KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Claim 15; Page 64; 88pp; English.
XX
CC The present sequence represents a cancer peptide that corresponds to
CC amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
CC AAY05965), a new and potent tumour antigen capable of eliciting an
CC antigen specific immune response by T cells. Cancer peptides derived from
CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
CC variants (see AAY05967-87), are useful as cancer vaccines that protect
CC against cancer. The invention provides: vectors and host cells (also
CC useful as vaccines); a method of diagnosis of cancer or precancer; a
CC transgenic animal; antisense oligonucleotides that inhibit expression of
CC the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
CC cancer peptide, useful in diagnostic and detection assays; and methods
CC for preventing or inhibiting cancer by administering a cancer peptide,
CC with or without an HLA molecule. The cancer peptides form part of, or are
CC derived from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
CC treated by inducing cancer-specific T cells in vitro for subsequent
CC return to a patient
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 55; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
||||||||||
Db 6 ASGPGGGAPR 15

RESULT 14
AAY05979
ID AAY05979 standard; peptide; 20 AA.
XX
AC AAY05979;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Claim 16; Page 64; 88pp; English.
XX
CC The present sequence represents a cancer peptide that is based on amino
CC acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965),
CC a new and potent tumour antigen capable of eliciting an antigen specific
CC immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-
CC 3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-
CC 87), are useful as cancer vaccines that protect against cancer. The
CC invention provides: vectors and host cells (also useful as vaccines); a
CC method of diagnosis of cancer or precancer; a transgenic animal;
CC antisense oligonucleotides that inhibit expression of the cancer peptide
CC or tumour antigen; antibodies reacting with a CAG-3 cancer peptide,
CC useful in diagnostic and detection assays; and methods for preventing or
CC inhibiting cancer by administering a cancer peptide, with or without an
CC HLA molecule. The cancer peptides form part of, or are derived from,
CC cancers such as primary or metastatic melanoma, thymoma, lymphoma,
CC sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
CC cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
CC prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by
CC inducing cancer-specific T cells in vitro for subsequent return to a
CC patient
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 55; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
||||||||||
Db 11 ASGPGGGAPR 20

RESULT 15
AAU85105
ID AAU85105 standard; peptide; 30 AA.
XX
AC AAU85105;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human NYNSO1a segment 4.
XX
KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW viral infection; human immunodeficieny virus; melanoma;
KW bacterial infection; Salmonella; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
XX
OS Homo sapiens.
XX

PN WO200190197-A1.
XX
PD 29-NOV-2001.
XX
PF 25-MAY-2001; 2001WO-AU000622.
XX
PR 26-MAY-2000; 2000AU-00007761.
XX
PA (AUSU) UNIV AUSTRALIAN NAT.
XX
PI Thomson SA, Ramshaw IA;
XX
DR WPI; 2002-147575/19.
DR N-PSDB; ABK36925.
XX
PT New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
PS Example 3; Fig 27; 364pp; English.
XX
CC The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention
XX
SQ Sequence 30 AA;

Query Match 100.0%; Score 55; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ASGPGGGAPR 10
              ||||||||||
Db         10 ASGPGGGAPR 19
```

Search completed: March 13, 2006, 19:03:58
Job time : 77.2941 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:04:24 ; Search time 11.8824 Seconds
(without alignments)
80.975 Million cell updates/sec

Title: US-09-529-206E-25
Perfect score: 55
Sequence: 1 ASGPGGGAPR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	44	80.0	3190	2	T13828	CREB-binding prote
2	42	76.4	378	2	C87425	aldose 1-epimerase
3	41	74.5	173	2	AB3648	flagellar basal-bo
4	41	74.5	286	2	S04673	H+-transporting tw
5	41	74.5	357	2	F82878	XAA-PRO aminopepti
6	41	74.5	1207	2	T00378	KIAA0641 protein -
7	40	72.7	335	2	S08341	myristylated alani
8	40	72.7	436	2	T36104	conserved hypothet
9	40	72.7	521	2	A29345	steroid hormone re
10	40	72.7	679	2	S02165	regulatory protein
11	40	72.7	954	2	A87431	regulatory protein
12	39	70.9	103	2	C72683	hypothetical prote
13	39	70.9	114	2	B45036	Pur beta - human (
14	39	70.9	163	2	E87464	competence/damage-
15	39	70.9	166	2	I69006	histocompatibility
16	39	70.9	187	2	T35619	hypothetical prote
17	39	70.9	260	2	F95899	probable transcrip
18	39	70.9	466	2	F95307	conserved hypothet
19	39	70.9	474	2	G75580	conserved hypothet
20	39	70.9	566	2	T34842	probable transfera
21	39	70.9	575	2	S35327	protein kinase sgg
22	39	70.9	627	2	T35608	polyketide hydroxy
23	39	70.9	733	2	S10932	probable protein k
24	39	70.9	757	2	JC7726	(1->4)-alpha-D-glu
25	39	70.9	1028	2	A56038	DNA-binding protei
26	39	70.9	1067	2	S35423	protein kinase sgg
27	39	70.9	1213	2	S16356	ovo protein - frui
28	39	70.9	1317	2	T03748	apoptosis associat
29	38	69.1	131	2	C75445	Pex-related protei
30	38	69.1	161	2	S12246	anther-specific pr
31	38	69.1	189	2	AE3136	Hypothetical Prote
32	38	69.1	189	2	G98151	hypothetical prote
33	38	69.1	201	2	C40040	alternative splici
34	38	69.1	201	2	S26404	alternative splici
35	38	69.1	248	2	A40040	alternative splici
36	38	69.1	286	2	T51008	related to antifre
37	38	69.1	292	2	B40040	alternative splici
38	38	69.1	316	2	AC1965	proline iminopepti
39	38	69.1	327	2	T29031	hypothetical prote
40	38	69.1	331	2	S78452	POU-domain protein
41	38	69.1	341	2	T08459	hypothetical prote
42	38	69.1	341	2	T48847	syntaxin synt4 [im
43	38	69.1	354	2	I80170	class I histocompa
44	38	69.1	397	2	T30168	hypothetical prote
45	38	69.1	420	2	I59234	octamer binding tr

ALIGNMENTS

RESULT 1
T13828
CREB-binding protein homolog - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13828
R;Akimaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; G
Nature 386, 735-738, 1997
A;Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling
A;Reference number: Z17785; MUID:97263578; PMID:9109493
A;Accession: T13828
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3190 <AKI>
A;Cross-references: UNIPROT:O01368; UNIPARC:UPI000003EB83; EMBL:U88570; NID:g1916929; P
C;Genetics:
A;Cross-references: FlyBase:FBgn0015624
A;Map position: X
F;1723-1780/Domain: bromodomain homology <BRO>

Query Match 80.0%; Score 44; DB 2; Length 3190;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SGPGGGAPR 10
:|||||.||
Db 320 NGPGGGGPR 328

RESULT 2
C87425
aldose 1-epimerase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: C87425
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87425
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-378 <STO>
A;Cross-references: UNIPROT:Q9A8D6; UNIPARC:UPI00000C73A0; GB:AE005673; NID:g13422779;
C;Genetics:
A;Gene: CC1418
C;Superfamily: aldose 1-epimerase

Query Match 76.4%; Score 42; DB 2; Length 378;
Best Local Similarity 77.8%; Pred. No. 56;

```
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 SGPGGGAPR 10
              :|| |||||
Db        282 NGPSGGAPR 290


RESULT 3
AB3648
flagellar basal-body rod protein flgF [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AB3648
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AB3648
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <KUR>
A;Cross-references: UNIPROT:Q8YAZ4; UNIPARC:UPI0000058740; GB:AE008918; PIDN:AAL54349.1;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII1107
A;Map position: II

  Query Match             74.5%;  Score 41;  DB 2;  Length 173;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 PGGGAPR 10
              |||||||
Db        132 PGGGAPR 138


RESULT 4
S04673
H+-transporting two-sector ATPase (EC 3.6.3.14) gamma chain - Rhodopseudomonas blastica
C;Species: Rhodopseudomonas blastica
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 31-Dec-2004
C;Accession: S04673
R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A;Title: Rhodopseudomonas blastica atp operon. Nucleotide sequence and transcription.
A;Reference number: S04666; MUID:85058188; PMID:6209404
A;Accession: S04673
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-286 <TYB>
A;Cross-references: UNIPROT:P05436; UNIPARC:UPI0000126582
C;Superfamily: H(+)-transporting ATP synthase gamma chain
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

  Query Match             74.5%;  Score 41;  DB 2;  Length 286;
  Best Local Similarity   80.0%;  Pred. No. 61;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||| | ||||
Db         57 ASGQGAGAPR 66


RESULT 5
F82878
XAA-PRO aminopeptidase UU532 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: F82878
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Reference number: A82870
A;Accession: F82878
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <GLA>
A;Cross-references: UNIPARC:UPI00000C1CAC; GB:AE002152; GB:AF222894; NID:g6899532; PIDN
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: pepP; UU532
A;Genetic code: SGC3
C;Superfamily: X-Pro aminopeptidase

  Query Match             74.5%;  Score 41;  DB 2;  Length 357;
  Best Local Similarity   77.8%;  Pred. No. 74;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAP 9
              |||| ||:|
Db        193 ASGPNGGSP 201


RESULT 6
T00378
KIAA0641 protein - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Accession: T00378
R;Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N
DNA Res. 5, 169-176, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. X. The completc
A;Reference number: Z14142; MUID:98403880; PMID:9734811
A;Accession: T00378
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1207 <ISH>
A;Cross-references: UNIPARC:UPI0000046CF7; EMBL:AB014541; NID:g3327095; PIDN:BAA31616.1,
C;Genetics:
A;Gene: KIAA0641

  Query Match             74.5%;  Score 41;  DB 2;  Length 1207;
  Best Local Similarity   70.0%;  Pred. No. 2.1e+02;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              |:|| || ||
Db        757 ATGPSGGQPR 766


RESULT 7
S08341
myristylated alanine-rich protein kinase C substrate - bovine
N;Alternate names: acidic calmodulin-binding 81K protein (ACAMP-81); MARCKS
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S08341; A32904; S29270; A46098; PS0338
R;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
Nucleic Acids Res. 17, 3987-3988, 1989
A;Title: Nucleotide sequence of a cDNA for the bovine myristoylated alanine-rich C kinas
A;Reference number: S08341; MUID:89282412; PMID:2734111
A;Accession: S08341
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-335 <STU>
A;Cross-references: UNIPROT:P12624; UNIPARC:UPI000016C340; EMBL:M24638; NID:g163339; PII
R;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 4012-4016, 1989
A;Title: Molecular cloning, characterization, and expression of a cDNA encoding the "80-
A;Reference number: A32904; MUID:89264553; PMID:2726763
A;Accession: A32904
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-98,'Q',100-335 <ST2>
A;Cross-references: UNIPARC:UPI000017750A; GB:M24638; GB:M23738
```

R;Herget, T.; Brooks, S.F.; Broad, S.; Rozengurt, E.
Eur. J. Biochem. 209, 7-14, 1992
A;Title: Relationship between the major protein kinase C substrates acidic 80-kDa protei
or equivalent genes in different species.
A;Reference number: S29267; MUID:93011168; PMID:1396720
A;Accession: S29270
A;Molecule type: DNA
A;Residues: 191-253,'SEE',257-279,283-292,'V',294,'PEQE',299,'A',300,'A',302-313,'A',315
A;Cross-references: UNIPARC:UPI000017750B
R;Manenti, S.; Sorokine, O.; Van Dorsselaer, A.; Taniguchi, H.
J. Biol. Chem. 268, 6878-6881, 1993
A;Title: Isolation of the non-myristoylated form of a major substrate of protein kinase
A;Reference number: A46098; MUID:93216617; PMID:8463217
A;Accession: A46098
A;Molecule type: protein
A;Residues: 2-11 <MAN>
A;Cross-references: UNIPARC:UPI000017750C
R;Mizutani, A.; Tokumitsu, H.; Hidaka, H.
Biochem. Biophys. Res. Commun. 182, 1395-1401, 1992
A;Title: Acidic calmodulin binding protein, ACAMP-81, is MARCKS protein interacting with
A;Reference number: PS0338; MUID:92171958; PMID:1540183
A;Accession: PS0338
A;Molecule type: protein
A;Residues: 12-30;56-69;88-98,'AS',100-103;104-109,'E',111-123;156-160;165-171;196-215;2
A;Cross-references: UNIPARC:UPI000017750D; UNIPARC:UPI000017750E; UNIPARC:UPI000017750F;
514
A;Experimental source: brain
A;Note: this sequence is identical with that of myristoylated alanine-rich C-kinase subs
C;Comment: This protein is a major cellular substrate for protein kinase C and plays a r
C;Comment: It binds to calmodulin in one to one molar ratio in the presence of calcium a
C;Genetics:
A;Introns: 34/3
C;Superfamily: neurofilament triplet H protein
C;Keywords: actin binding; blocked amino end; calmodulin binding; lipoprotein; myristyla
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;158,162,166,169/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status

Query Match 72.7%; Score 40; DB 2; Length 335;
Best Local Similarity 64.3%; Pred. No. 98;
Matches 9; Conservative 1; Mismatches 0; Indels 4; Gaps 1;

Qy 1 ASGPG----GGAPR 10
|:||| |||||
Db 288 AAGPGCPRAGGAPR 301

RESULT 8
T36104
conserved hypothetical protein SCE15.01 - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36104
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1999
A;Reference number: Z21597
A;Accession: T36104
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-436 <MUR>
A;Cross-references: UNIPROT:Q8CJX1; UNIPARC:UPI000017AD99; EMBL:AL049707; PIDN:CAB41270.
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCE15.01

Query Match 72.7%; Score 40; DB 2; Length 436;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASGPGGGAP 9
|||||| |
Db 153 ASGPGGNTP 161

RESULT 9
A29345
steroid hormone receptor ERR1 precursor - human
N;Alternate names: estrogen-related receptor
C;Species: Homo sapiens (man)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 31-Dec-2004
C;Accession: A29345; A49074
R;Giguere, V.; Yang, N.; Segui, P.; Evans, R.M.
Nature 331, 91-94, 1988
A;Title: Identification of a new class of steroid hormone receptors.
A;Reference number: A29345; MUID:88122546; PMID:3267207
A;Accession: A29345
A;Molecule type: mRNA
A;Residues: 1-521 <GIG>
A;Cross-references: UNIPROT:P11474; UNIPARC:UPI0000142399; EMBL:X51416; NID:g36608; PID
R;Wiley, S.R.; Kraus, R.J.; Zuo, F.; Murray, E.E.; Loritz, K.; Mertz, J.E.
Genes Dev. 7, 2206-2219, 1993
A;Title: SV40 early-to-late switch involves titration of cellular transcriptional repre
A;Reference number: A49074; MUID:94040741; PMID:8224847
A;Accession: A49074
A;Status: preliminary
A;Molecule type: protein
A;Residues: 166-169,'X',171-173 <WIL>
A;Cross-references: UNIPARC:UPI000017A1DF
C;Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; z
F;174-434/Domain: erbA transforming protein homology <ERBA>
F;176-196/Region: zinc finger
F;212-236/Region: zinc finger

Query Match 72.7%; Score 40; DB 2; Length 521;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SGPGGGAPR 10
:|||||| |
Db 465 AGPGGGAER 473

RESULT 10
S02165
regulatory protein flaY - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S02165
R;Kaplan, J.B.; Dingwall, A.; Bryan, R.; Champer, R.; Shapiro, L.
J. Mol. Biol. 205, 71-83, 1989
A;Title: Temporal regulation and overlap organization of two Caulobacter flagellar gene
A;Reference number: S02164; MUID:89178645; PMID:2648000
A;Accession: S02165
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-679 <KAP>
A;Cross-references: UNIPROT:P15345; UNIPARC:UPI000017A8F7
C;Genetics:
A;Gene: flaY
C;Keywords: transcription regulation

Query Match 72.7%; Score 40; DB 2; Length 679;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASGPGGGAP 9
| ||| |||
Db 173 AGGPGAGAP 181

RESULT 11
A87431
regulatory protein FlaEY [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87431
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87431
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-954 <STO>
A;Cross-references: UNIPROT:P15345; UNIPARC:UPI000012A8ED; GB:AE005673; NID:g13422833; P
C;Genetics:
A;Gene: CC1465

  Query Match 72.7%; Score 40; DB 2; Length 954;
  Best Local Similarity 77.8%; Pred. No. 2.4e+02;
  Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASGPGGGAP 9
  | ||| |||
Db 317 AGGPGAGAP 325

RESULT 12
C72683
hypothetical protein APE0884 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: C72683
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: C72683
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-103 <KAW>
A;Cross-references: UNIPROT:Q9YDN0; UNIPARC:UPI000005DD18; DDBJ:AP000060; NID:g5104188;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0884

  Query Match 70.9%; Score 39; DB 2; Length 103;
  Best Local Similarity 85.7%; Pred. No. 49;
  Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GPGGGAP 9
  |||||:|
Db 21 GPGGGSP 27

RESULT 13
B45036
Pur beta - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B45036
R;Bergemann, A.D.; Ma, Z.W.; Johnson, E.M.
Mol. Cell. Biol. 12, 5673-5682, 1992
A;Title: Sequence of cDNA comprising the human pur gene and sequence-specific single-str
A;Reference number: B45036; MUID:93078769; PMID:1448097
A;Accession: B45036
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-114 <BER>
A;Cross-references: UNIPROT:Q96QR8; UNIPARC:UPI000017C32D
A;Experimental source: HeLa cells
A;Note: sequence extracted from NCBI backbone (NCBIP:119218)

  Query Match 70.9%; Score 39; DB 2; Length 114;
  Best Local Similarity 87.5%; Pred. No. 54;
  Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASGPGGGA 8
  | ||||||
Db 3 AGGPGGGA 10

RESULT 14
E87464
competence/damage-inducible protein CinA [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 05-Oct-2004
C;Accession: E87464
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87464
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-163 <STO>
A;Cross-references: UNIPROT:Q9A7I6; UNIPARC:UPI00000C74AD; GB:AE005673; NID:g13423155; P
C;Genetics:
A;Gene: CC1737
C;Superfamily: uncharacterized protein related to CinA

  Query Match 70.9%; Score 39; DB 2; Length 163;
  Best Local Similarity 75.0%; Pred. No. 73;
  Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SGPGGGAP 9
  :||||| |
Db 106 AGPGGGTP 113

RESULT 15
I69006
histocompatibility antigen - rhesus macaque (fragment)
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: I69006
R;Boyson, J.E.; McAdam, S.N.; Gallimore, A.; Golos, T.G.; Liu, X.; Gotch, F.M.; Hughes,
Immunogenetics 41, 59-68, 1995
A;Title: The MHC E locus in macaques is polymorphic and is conserved between macaques an
A;Reference number: I54551; MUID:95104933; PMID:7806297
A;Accession: I69006
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-166 <RES>
A;Cross-references: UNIPROT:Q95518; UNIPARC:UPI00000892D6; EMBL:U02981; NID:g532971; PIR
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

  Query Match 70.9%; Score 39; DB 2; Length 166;
  Best Local Similarity 77.8%; Pred. No. 74;
  Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SGPGGGAPR 10
  | |||| ||
Db 5 SRPGGGGPR 13

Search completed: March 13, 2006, 19:16:08
Job time : 13.8824 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 18:53:23 ; Search time 72.5882 Seconds
(without alignments)
97.196 Million cell updates/sec

Title: US-09-529-206E-25
Perfect score: 55
Sequence: 1 ASGPGGGAPR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	100.0	142	2	Q9NY13_HUMAN	Q9ny13 homo sapien
2	55	100.0	180	1	CTG1B_HUMAN	P78358 homo sapien
3	55	100.0	180	2	Q7LBY4_HUMAN	Q7lby4 homo sapien
4	47	85.5	210	1	CTAG2_HUMAN	O75638 homo sapien
5	46	83.6	327	2	Q63HT9_BURPS	Q63ht9 burkholderi
6	46	83.6	330	2	Q629N3_BURMA	Q629n3 burkholderi
7	46	83.6	708	2	Q5KJM5_CRYNE	Q5kjm5 cryptococcu
8	46	83.6	708	2	Q55WM1_CRYNE	Q55wm1 cryptococcu
9	45	81.8	309	2	Q63N33_BURPS	Q63n33 burkholderi
10	45	81.8	362	2	Q63QT8_BURPS	Q63qt8 burkholderi
11	45	81.8	362	2	Q62H22_BURMA	Q62h22 burkholderi
12	45	81.8	788	2	Q4QQP8_HUMAN	Q4qqp8 homo sapien
13	44	80.0	262	2	Q4NUZ3_9DELT	Q4nuz3 anaeromyxob
14	44	80.0	271	2	Q4NAC6_9MICC	Q4nac6 arthrobacte
15	44	80.0	367	2	Q6AV33_ORYSA	Q6av33 oryza sativ
16	44	80.0	398	2	Q8N6H2_HUMAN	Q8n6h2 homo sapien
17	44	80.0	398	2	Q5SQU1_HUMAN	Q5squ1 homo sapien
18	44	80.0	399	2	Q8IVQ3_HUMAN	Q8ivq3 homo sapien
19	44	80.0	492	2	Q7NWI2_CHRVO	Q7nwi2 chromobacte
20	44	80.0	566	2	Q5SQT4_HUMAN	Q5sqt4 homo sapien
21	44	80.0	584	2	Q5P6Z0_AZOSE	Q5p6z0 azoarcus sp
22	44	80.0	3190	2	O01368_DROME	O01368 drosophila
23	44	80.0	3276	2	Q9W321_DROME	Q9w321 drosophila
24	43	78.2	108	2	Q8H321_ORYSA	Q8h321 oryza sativ
25	43	78.2	218	2	Q69PJ1_ORYSA	Q69pj1 oryza sativ
26	43	78.2	218	2	Q69PJ3_ORYSA	Q69pj3 oryza sativ
27	43	78.2	230	2	Q6YPC1_ORYSA	Q6ypc1 oryza sativ
28	43	78.2	270	2	Q6UU54_ORYSA	Q6uu54 oryza sativ
29	43	78.2	322	2	Q67PJ0_SYMTH	Q67pj0 symbiobacte
30	43	78.2	342	2	Q9SP09_TOBAC	Q9sp09 nicotiana t
31	43	78.2	392	2	Q6GLG9_XENTR	Q6glg9 xenopus tro
32	43	78.2	500	2	Q6UU52_ORYSA	Q6uu52 oryza sativ
33	43	78.2	560	2	Q4ILQ5_GIBZE	Q4ilq5 gibberella
34	43	78.2	564	2	Q96TZ3_NEUCR	Q96tz3 neurospora
35	43	78.2	571	2	Q4WRL3_ASPFU	Q4wrl3 aspergillus
36	43	78.2	574	2	Q5BEV2_EMENI	Q5bev2 aspergillus
37	43	78.2	640	2	Q6ZV16_HUMAN	Q6zv16 homo sapien
38	43	78.2	811	2	Q5K4L6_HUMAN	Q5k416 homo sapien
39	43	78.2	811	2	Q5VUQ8_HUMAN	Q5vuq8 homo sapien
40	43	78.2	1000	2	Q4FKF7_9TRYP	Q4fkf7 trypanosoma
41	43	78.2	1383	2	Q4SW43_TETNG	Q4sw43 tetraodon n
42	42	76.4	194	2	Q96BU2_HUMAN	Q96bu2 homo sapien
43	42	76.4	217	2	Q4SYU9_TETNG	Q4syu9 tetraodon n
44	42	76.4	344	2	Q4TGY6_TETNG	Q4tgy6 tetraodon n
45	42	76.4	355	2	Q9H8E2_HUMAN	Q9h8e2 homo sapien

ALIGNMENTS

RESULT 1
Q9NY13_HUMAN
ID Q9NY13_HUMAN PRELIMINARY; PRT; 142 AA.
AC Q9NY13;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein LAGE-2 (Fragment).
GN Name=LAGE-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ275978; CAB76945.1; -; mRNA.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;

Query Match 100.0%; Score 55; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
||||||||||
Db 27 ASGPGGGAPR 36

RESULT 2
CTG1B_HUMAN
ID CTG1B_HUMAN STANDARD; PRT; 180 AA.
AC P78358;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-
DE ESO-1).
GN Name=CTAG1B; Synonyms=CTAG, CTAG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
RA Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,
RA Williamson B., Stockert E., Pfreundschuh M., Old L.J.;
RT "A testicular antigen aberrantly expressed in human cancers detected
RT by autologous antibody screening.";

```
RL   Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Melanoma;
RX   MEDLINE=98289662; PubMed=9626360;
RA   Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA   de Plaen E., Boon T.;
RT   "LAGE-1, a new gene with tumor specificity.";
RL   Int. J. Cancer 76:903-908(1998).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98430682; PubMed=9759882;
RA   Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,
RA   Schwartzentruber D.J., Rosenberg S.A.;
RT   "A breast and melanoma-shared tumor antigen: T cell responses to
RT   antigenic peptides translated from different open reading frames.";
RL   J. Immunol. 161:3596-3606(1998).
CC   -!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide
CC       variety of cancers. Detected in uterine myometrium.
CC   -!- SIMILARITY: Belongs to the CTAG family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U87459; AAB49693.1; -; mRNA.
DR   EMBL; AJ003149; CAA05908.1; -; mRNA.
DR   EMBL; AF038567; AAD05202.1; -; mRNA.
DR   HGNC; HGNC:2491; CTAG1B.
DR   MIM; 300156; -.
KW   Antigen; Transmembrane.
FT   TRANSMEM    156    172       Potential.
FT   COMPBIAS      5     82       Gly-rich.
SQ   SEQUENCE   180 AA;  17992 MW;  B122C5C2C8BE1569 CRC64;

  Query Match             100.0%;  Score 55;  DB 1;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 2;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db         53 ASGPGGGAPR 62


RESULT 3
Q7LBY4_HUMAN
ID   Q7LBY4_HUMAN PRELIMINARY;      PRT;   180 AA.
AC   Q7LBY4;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
DE   antigen 1-A).
GN   Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21303268;
RA   Galgoczy P., Rosenthal A., Platzer M.;
RT   "Human-mouse comparative sequence analysis of the NEMO gene reveals an
RT   alternative promoter within the neighboring G6PD gene.";
RL   Gene 271:93-98(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21566154; PubMed=11709543; DOI=10.1093/hmg/10.22.2557;
RA   Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
RA   Patlan H., Ciccodicola A., Kenwrick S., Platzer M., D'Urso M.,
RA   Nelson D.L.;
RT   "Multiple pathogenic and benign genomic rearrangements occur at a 35
RT   kb duplication involving the NEMO and LAGE2 genes.";
RL   Hum. Mol. Genet. 10:2557-2567(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Platzer M.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Platzer M.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RA   Galgoczy P., Platzer M.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99454989; PubMed=10523621;
RA   De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
RT   "DNA methylation is the primary silencing mechanism for a set of germ
RT   line- and tumor-specific genes with a CpG-rich promoter.";
RL   Mol. Cell. Biol. 19:7327-7335(1999).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RA   Lethe B.G.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF277315; AAL27014.1; -; Genomic_DNA.
DR   EMBL; AJ275977; CAB76943.1; -; Genomic_DNA.
DR   EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
SQ   SEQUENCE   180 AA;  17992 MW;  B122C5C2C8BE1569 CRC64;

  Query Match             100.0%;  Score 55;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 2;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db         53 ASGPGGGAPR 62


RESULT 4
CTAG2_HUMAN
ID   CTAG2_HUMAN    STANDARD;      PRT;   210 AA.
AC   O75638; O75637; Q9BU80; Q9UJ89; Q9Y479;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
GN   Name=CTAG2; Synonyms=ESO2, LAGE1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B).
RC   TISSUE=Melanoma;
RX   MEDLINE=98289662; PubMed=9626360;
RA   Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA   de Plaen E., Boon T.;
RT   "LAGE-1, a new gene with tumor specificity.";
RL   Int. J. Cancer 76:903-908(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B), AND VARIANTS
RP   GLN-6; GLN-89 AND ARG-138.
RC   TISSUE=Melanoma;
RX   MEDLINE=99325550; PubMed=10399963;
RA   Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT   "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT   unexpected translation product of LAGE-1.";
RL   Int. J. Cancer 82:442-448(1999).
RN   [3]
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RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
RP   ARG-138.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=LAGE-1B; Synonyms=LAGE-1L;
CC         IsoId=O75638-1; Sequence=Displayed;
CC       Name=LAGE-1A; Synonyms=LAGE-1S;
CC         IsoId=O75638-2; Sequence=VSP_004301;
CC   -!- TISSUE SPECIFICITY: Testis and very low level in placenta and in
CC       some uterus samples. Observed in 25-50% of tumor samples of
CC       melanomas, non-small-cell lung carcinomas, bladder, prostate and
CC       head and neck cancers.
CC   -!- DOMAIN: A transmembrane domain is present in isoform LAGE-1A.
CC   -!- SIMILARITY: Belongs to the CTAG family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AJ223093; CAA11117.1; -; Genomic_DNA.
DR   EMBL; AJ223093; CAA11116.1; -; Genomic_DNA.
DR   EMBL; AJ223040; CAA11043.1; -; mRNA.
DR   EMBL; AJ223041; CAA11044.1; -; mRNA.
DR   EMBL; AJ012834; CAA10194.1; -; mRNA.
DR   EMBL; AJ012835; CAA10196.1; -; mRNA.
DR   EMBL; BC002833; AAH02833.1; -; mRNA.
DR   Ensembl; ENSG00000126890; Homo sapiens.
DR   HGNC; HGNC:2492; CTAG2.
DR   H-InvDB; HIX0017163; -.
DR   MIM; 300396; -.
KW   Alternative splicing; Antigen; Polymorphism; Transmembrane.
FT   COMPBIAS      5     79       Gly-rich.
FT   COMPBIAS    183    188       Poly-Pro.
FT   VARSPLIC    135    210       MSVWDQDREGAGRMRVVGWGLGSASPEGQKARDLRTPKHKV
FT                                SEQRPGTPGPPPPEGAQGDGCRGVAFNVMFSAPHI -> IR
FT                                LTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQAPSG
FT                                QRR (in isoform LAGE-1A).
FT                                /FTId=VSP_004301.
FT   VARIANT       6      6       R -> Q.
FT                                /FTId=VAR_007855.
FT   VARIANT      89     89       E -> Q.
FT                                /FTId=VAR_007856.
FT   VARIANT     138    138       W -> R.
FT                                /FTId=VAR_007857.
SQ   SEQUENCE   210 AA;  21120 MW;  8BE0EE00AE55E8BE CRC64;

  Query Match             85.5%;  Score 47;  DB 1;  Length 210;
  Best Local Similarity   90.0%;  Pred. No. 36;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              |||| |||||
Db         53 ASGPRGGAPR 62


RESULT 5
Q63HT9_BURPS
ID   Q63HT9_BURPS PRELIMINARY;      PRT;   327 AA.
AC   Q63HT9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative lipoprotein.
GN   OrderedLocusNames=BPSS2331;
OS   Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia; pseudomallei group.
OX   NCBI_TaxID=28450;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=K96243;
RX   PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA   Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
RA   Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA   Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
RA   Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA   Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D.,
RA   Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA   Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA   Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA   Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA   Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT   "Genomic plasticity of the causative agent of melioidosis,
RT   Burkholderia pseudomallei.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR   EMBL; BX571966; CAH39817.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR007428; VacJ.
DR   Pfam; PF04333; VacJ; 1.
DR   PRINTS; PR01805; VACJLIPOPROT.
KW   Complete proteome; Lipoprotein.
SQ   SEQUENCE   327 AA;  33687 MW;  AC5D2C7CC4A44A25 CRC64;

  Query Match             83.6%;  Score 46;  DB 2;  Length 327;
  Best Local Similarity   88.9%;  Pred. No. 78;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAP 9
              | |||||||
Db        243 AGGPGGGAP 251


RESULT 6
Q629N3_BURMA
ID   Q629N3_BURMA PRELIMINARY;      PRT;   330 AA.
AC   Q629N3;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative lipoprotein.
GN   OrderedLocusNames=BMAA2092;
OS   Burkholderia mallei (Pseudomonas mallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia.
OX   NCBI_TaxID=13373;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ATCC 23344;
RX   PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA   Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA   Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA   Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
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RA   Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA   Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
RA   Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA   Zafar N., Zhou L., Fraser C.M.;
RT   "Structural flexibility in the Burkholderia mallei genome.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR   EMBL; CP000011; AAU47030.1; -; Genomic_DNA.
DR   TIGR; BMAA2092; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR007428; VacJ.
DR   Pfam; PF04333; VacJ; 1.
DR   PRINTS; PR01805; VACJLIPOPROT.
KW   Complete proteome; Lipoprotein.
SQ   SEQUENCE   330 AA;  33977 MW;  2F12165CD7366835 CRC64;

  Query Match             83.6%;  Score 46;  DB 2;  Length 330;
  Best Local Similarity   88.9%;  Pred. No. 78;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAP 9
              | |||||||
Db        243 AGGPGGGAP 251


RESULT 7
Q5KJM5_CRYNE
ID   Q5KJM5_CRYNE PRELIMINARY;      PRT;   708 AA.
AC   Q5KJM5;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Actin cross-linking, putative.
GN   ORFNames=CNC06000;
OS   Cryptococcus neoformans var. neoformans JEC21.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC   Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX   NCBI_TaxID=214684;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=JEC21;
RA   Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,
RA   Van Aken S., Fraser C.;
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=JEC21;
RX   PubMed=15653466; DOI=10.1126/science.1103773;
RA   Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
RA   Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
RA   Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
RA   D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
RA   Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
RA   Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,
RA   Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L.,
RA   Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA   Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
RA   Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
RA   Fraser C.M., Hyman R.W.;
RT   "The genome of the basidiomycetous yeast and human pathogen
RT   Cryptococcus neoformans.";
RL   Science 307:1321-1324(2005).
DR   EMBL; AE017343; AAW42672.1; -; Genomic_DNA.
DR   GO; GO:0003779; F:actin binding; IEA.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   InterPro; IPR001589; Actnin_actin_bd.
DR   InterPro; IPR001715; Calponin_act_bd.
DR   InterPro; IPR011992; EF-Hand_type.
DR   InterPro; IPR002017; Spectrin.
DR   Pfam; PF00307; CH; 2.
DR   SMART; SM00033; CH; 2.
DR   PROSITE; PS00019; ACTININ_1; UNKNOWN_1.
DR   PROSITE; PS00020; ACTININ_2; 1.
DR   PROSITE; PS50021; CH; 2.
KW   Complete proteome.
SQ   SEQUENCE   708 AA;  79873 MW;  BAF52D1DD2C99B9D CRC64;

  Query Match             83.6%;  Score 46;  DB 2;  Length 708;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAP 9
              | |||||||
Db         47 AGGPGGGAP 55


RESULT 8
Q55WM1_CRYNE
ID   Q55WM1_CRYNE PRELIMINARY;      PRT;   708 AA.
AC   Q55WM1;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=CNBC1180;
OS   Cryptococcus neoformans var. neoformans B-3501A.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC   Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX   NCBI_TaxID=283643;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=B-3501A;
RA   Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
RA   Wickes B.L., Fu J., Davis R.W.;
RT   "Cryptococcus neoformans serotype D sequencing.";
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAEY01000013; EAL21978.1; -; Genomic_DNA.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   InterPro; IPR001589; Actnin_actin_bd.
DR   InterPro; IPR001715; Calponin_act_bd.
DR   InterPro; IPR011992; EF-Hand_type.
DR   InterPro; IPR002017; Spectrin.
DR   Pfam; PF00307; CH; 2.
DR   SMART; SM00033; CH; 2.
DR   PROSITE; PS00019; ACTININ_1; UNKNOWN_1.
DR   PROSITE; PS00020; ACTININ_2; UNKNOWN_1.
DR   PROSITE; PS50021; CH; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   708 AA;  79873 MW;  BAF52D1DD2C99B9D CRC64;

  Query Match             83.6%;  Score 46;  DB 2;  Length 708;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAP 9
              | |||||||
Db         47 AGGPGGGAP 55


RESULT 9
Q63N33_BURPS
ID   Q63N33_BURPS PRELIMINARY;      PRT;   309 AA.
AC   Q63N33;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putrescine transport system permease protein.
GN   Name=potI; OrderedLocusNames=BPSS0464;
OS   Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia; pseudomallei group.
OX   NCBI_TaxID=28450;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
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RC   STRAIN=K96243;
RX   PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA   Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
RA   Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA   Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
RA   Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA   Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D.,
RA   Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA   Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA   Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA   Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA   Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT   "Genomic plasticity of the causative agent of melioidosis,
RT   Burkholderia pseudomallei.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
CC   -!- FUNCTION: Part of a binding-protein-dependent transport system.
CC       Probably responsible for the translocation of the substrate across
CC       the membrane (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the binding-protein-dependent transport
CC       system permease family.
DR   EMBL; BX571966; CAH37920.1; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR000515; BPD_transp.
DR   Pfam; PF00528; BPD_transp_1; 1.
DR   PROSITE; PS50928; ABC_TM1; 1.
KW   Complete proteome; Transmembrane; Transport.
SQ   SEQUENCE   309 AA;  33544 MW;  379E21B5B31CDE30 CRC64;

  Query Match             81.8%;  Score 45;  DB 2;  Length 309;
  Best Local Similarity   88.9%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 SGPGGGAPR 10
              ||| |||||
Db        287 SGPAGGAPR 295


RESULT 10
Q63QT8_BURPS
ID   Q63QT8_BURPS PRELIMINARY;      PRT;   362 AA.
AC   Q63QT8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative DNA polymerase III.
GN   OrderedLocusNames=BPSL2936;
OS   Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia; pseudomallei group.
OX   NCBI_TaxID=28450;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=K96243;
RX   PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA   Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
RA   Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA   Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
RA   Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA   Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D.,
RA   Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA   Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA   Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA   Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA   Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT   "Genomic plasticity of the causative agent of melioidosis,
RT   Burkholderia pseudomallei.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR   EMBL; BX571965; CAH36946.1; -; Genomic_DNA.
DR   GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR   GO; GO:0006260; P:DNA replication; IEA.
DR   InterPro; IPR010372; DNA_pol3_delta.
DR   InterPro; IPR005790; DNA_polIII_delta.
DR   Pfam; PF06144; DNA_pol3_delta; 1.
DR   TIGRFAMs; TIGR01128; holA; 1.
KW   Complete proteome.
SQ   SEQUENCE   362 AA;  38726 MW;  D5FF3DE783D41E41 CRC64;

  Query Match             81.8%;  Score 45;  DB 2;  Length 362;
  Best Local Similarity   80.0%;  Pred. No. 1.2e+02;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
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Db        350 AAGPGGDAPR 359


RESULT 11
Q62H22_BURMA
ID   Q62H22_BURMA PRELIMINARY;      PRT;   362 AA.
AC   Q62H22;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   DNA polymerase III, delta subunit (EC 2.7.7.7).
GN   Name=holA; OrderedLocusNames=BMA2451;
OS   Burkholderia mallei (Pseudomonas mallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia.
OX   NCBI_TaxID=13373;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ATCC 23344;
RX   PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA   Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA   Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA   Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA   Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA   Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
RA   Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA   Zafar N., Zhou L., Fraser C.M.;
RT   "Structural flexibility in the Burkholderia mallei genome.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR   EMBL; CP000010; AAU49707.1; -; Genomic_DNA.
DR   TIGR; BMA2451; -.
DR   GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006260; P:DNA replication; IEA.
DR   InterPro; IPR010372; DNA_pol3_delta.
DR   InterPro; IPR005790; DNA_polIII_delta.
DR   Pfam; PF06144; DNA_pol3_delta; 1.
DR   TIGRFAMs; TIGR01128; holA; 1.
KW   Complete proteome; Nucleotidyltransferase; Transferase.
SQ   SEQUENCE   362 AA;  38726 MW;  D5FF3DE783D41E41 CRC64;

  Query Match             81.8%;  Score 45;  DB 2;  Length 362;
  Best Local Similarity   80.0%;  Pred. No. 1.2e+02;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              |:|||| |||
Db        350 AAGPGGDAPR 359


RESULT 12
Q4QQP8_HUMAN
ID   Q4QQP8_HUMAN PRELIMINARY;      PRT;   788 AA.
AC   Q4QQP8;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   PTGFRN protein (Fragment).
GN   Name=PTGFRN;
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OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RG   NIH MGC Project;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC098142; AAH98142.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 5.
DR   PROSITE; PS50835; IG_LIKE; 4.
FT   NON_TER       1       1
SQ   SEQUENCE   788 AA;  88279 MW;  F49E034EE2D3603B CRC64;

  Query Match          81.8%;  Score 45;  DB 2;  Length 788;
  Best Local Similarity   88.9%;  Pred. No. 2.6e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAP 9
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Db          7 ARGPGGGAP 15


RESULT 13
Q4NUZ3_9DELT
ID   Q4NUZ3_9DELT PRELIMINARY;      PRT;   262 AA.
AC   Q4NUZ3;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Translation initiation factor 2.
GN   ORFNames=AdehDRAFT_2230;
OS   Anaeromyxobacter dehalogenans 2CP-C.
OC   Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC   Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
OX   NCBI_TaxID=290397;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=2CP-C;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome assembly of Anaeromyxobacter
RT   dehalogenans 2CP-C.";
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=2CP-C;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Anaeromyxobacter
RT   dehalogenans 2CP-C.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAHD01000012; EAL79408.1; -; Genomic_DNA.
KW   Initiation factor.
SQ   SEQUENCE   262 AA;  25294 MW;  7EF93CC8DE0B47FF CRC64;

  Query Match          80.0%;  Score 44;  DB 2;  Length 262;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GPGGGAPR 10
              |||||||:
Db        254 GPGGGAPK 261


RESULT 14
Q4NAC6_9MICC
ID   Q4NAC6_9MICC PRELIMINARY;      PRT;   271 AA.
AC   Q4NAC6;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=ArthDRAFT_0388;
OS   Arthrobacter sp. FB24.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Micrococcineae; Micrococcaceae; Arthrobacter.
OX   NCBI_TaxID=290399;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FB24;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome assembly of Arthrobacter sp. FB24.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FB24;
RG   US DOE Joint Genome Institute (PGF-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Arthrobacter sp. FB24.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAHG01000033; EAL94269.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   271 AA;  29989 MW;  5ECC048B06CDD5BA CRC64;

  Query Match          80.0%;  Score 44;  DB 2;  Length 271;
  Best Local Similarity   87.5%;  Pred. No. 1.3e+02;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GPGGGAPR 10
              |||||||:
Db         75 GPGGGAPK 82


RESULT 15
Q6AV33_ORYSA
ID   Q6AV33_ORYSA PRELIMINARY;      PRT;   367 AA.
AC   Q6AV33;
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DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein OSJNBa0063J18.9.
GN   Name=OSJNBa0063J18.9;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA   Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA   Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA   Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA   Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA   White O., Salzberg S.L., Fraser C.M.;
RT   "Oryza sativa chromosome 3 BAC OSJNBa0063J18 genomic sequence.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell R.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC107206; AAT77052.1; -; Genomic_DNA.
DR   Gramene; Q6AV33; -.
KW   Hypothetical protein.
SQ   SEQUENCE   367 AA;  37474 MW;  B8C62D9D4CC18C86 CRC64;

  Query Match             80.0%;  Score 44;  DB 2;  Length 367;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+02;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
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Db         94 ASGPGGGSAR 103


Search completed: March 13, 2006, 19:14:23
Job time : 74.5882 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:14:49 ; Search time 18.5882 Seconds
(without alignments)
44.477 Million cell updates/sec

Title: US-09-529-206E-25
Perfect score: 55
Sequence: 1 ASGPGGGAPR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	100.0	180	1	US-08-791-495-9	Sequence 9, Appli
2	55	100.0	180	2	US-08-937-263B-8	Sequence 8, Appli
3	55	100.0	180	2	US-09-751-798-8	Sequence 8, Appli
4	55	100.0	180	2	US-09-392-714-25	Sequence 25, Appl
5	55	100.0	180	2	US-09-165-546D-15	Sequence 15, Appl
6	55	100.0	180	2	US-09-341-829A-9	Sequence 9, Appli
7	55	100.0	180	2	US-09-849-602-30	Sequence 30, Appl
8	47	85.5	180	1	US-08-791-495-7	Sequence 7, Appli
9	47	85.5	180	2	US-09-341-829A-7	Sequence 7, Appli
10	47	85.5	210	1	US-08-791-495-5	Sequence 5, Appli
11	47	85.5	210	2	US-09-341-829A-5	Sequence 5, Appli
12	45	81.8	421	2	US-09-252-991A-32326	Sequence 32326, A
13	43	78.2	9	2	US-09-344-040C-117	Sequence 117, App
14	43	78.2	9	2	US-09-833-039A-117	Sequence 117, App
15	43	78.2	210	2	US-09-252-991A-24923	Sequence 24923, A
16	43	78.2	809	2	US-09-252-991A-31759	Sequence 31759, A
17	42	76.4	160	2	US-09-252-991A-17249	Sequence 17249, A
18	42	76.4	283	2	US-09-252-991A-17831	Sequence 17831, A
19	42	76.4	836	2	US-09-491-356C-21	Sequence 21, Appl
20	42	76.4	1427	2	US-09-252-991A-20577	Sequence 20577, A
21	41	74.5	143	2	US-08-789-329C-10	Sequence 10, Appl
22	41	74.5	172	2	US-08-789-329C-7	Sequence 7, Appli
23	41	74.5	175	2	US-08-789-329C-3	Sequence 3, Appli
24	41	74.5	340	2	US-09-949-002-562	Sequence 562, App
25	41	74.5	412	1	US-08-878-989-6	Sequence 6, Appli
26	41	74.5	412	2	US-09-272-796-6	Sequence 6, Appli
27	41	74.5	536	2	US-09-270-767-43766	Sequence 43766, A
28	41	74.5	555	2	US-10-104-047-3369	Sequence 3369, Ap
29	41	74.5	679	2	US-09-252-991A-27111	Sequence 27111, A
30	41	74.5	807	2	US-09-252-991A-32992	Sequence 32992, A
31	41	74.5	1000	2	US-09-252-991A-31361	Sequence 31361, A
32	41	74.5	1207	2	US-10-098-600B-16	Sequence 16, Appl
33	41	74.5	1207	2	US-09-949-002-376	Sequence 376, App
34	41	74.5	1323	2	US-09-248-796A-19543	Sequence 19543, A
35	41	74.5	1384	2	US-08-976-255-11	Sequence 11, Appl
36	40	72.7	137	2	US-09-252-991A-20489	Sequence 20489, A
37	40	72.7	174	2	US-09-902-540-12423	Sequence 12423, A
38	40	72.7	291	2	US-09-902-540-15052	Sequence 15052, A
39	40	72.7	335	1	US-08-405-175A-6	Sequence 6, Appli
40	40	72.7	424	2	US-09-252-991A-20642	Sequence 20642, A
41	40	72.7	438	2	US-09-949-016-7812	Sequence 7812, Ap
42	40	72.7	502	2	US-10-088-045-2	Sequence 2, Appli
43	40	72.7	502	2	US-10-088-045-4	Sequence 4, Appli
44	40	72.7	505	1	US-08-660-765A-2	Sequence 2, Appli
45	40	72.7	518	1	US-08-836-620A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth , Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 55; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ASGPGGGAPR 10
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Db         53 ASGPGGGAPR 62
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RESULT 2
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
;  GENERAL INFORMATION:
;    APPLICANT:  Chen, Yao-Tseng; Scanlan, Matthew;
;    APPLICANT:  Gure, Ali; Old, Lloyd J.; Jager, Elke;
;    APPLICANT:  Alexander, Knuth; Drijfhout, Jan W.
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULE
;    TITLE OF INVENTION:  ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
;    TITLE OF INVENTION:  ITSELF, AND USES THEREOF
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/937,263B
;      FILING DATE:  September 15, 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sinn, Eric, Patent Agent
;      REGISTRATION NUMBER:  40,177
;      REFERENCE/DOCKET NUMBER:  LUD 5466.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3000
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-937-263B-8

  Query Match             100.0%;  Score 55;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db         53 ASGPGGGAPR 62


RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
;  GENERAL INFORMATION:
;    APPLICANT:  Stockert, Elisabeth; Jager, Elke;
;    APPLICANT:  Chen, Yao-tseng; Scanlan, Matthew;
;    APPLICANT:  Knuth, Alexander; Old, Lloyd J.
;    TITLE OF INVENTION:  Antibodies Which Bind to NY-ESO-1 Cancer
;    TITLE OF INVENTION:  Associated Proteins, Uses Thereof,
;    TITLE OF INVENTION:  Truncated Forms of NY-ESO-1, and HLA
;    TITLE OF INVENTION:  Binding Peptides Derived Therefrom
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/751,798
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/062,422
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 6525177man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3168
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-09-751-798-8

  Query Match             100.0%;  Score 55;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db         53 ASGPGGGAPR 62


RESULT 4
US-09-392-714-25
; Sequence 25, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT: Gure, Ali O.
;  APPLICANT: Williamson, Barbara
;  APPLICANT: Chen, Yao-Tseng
;  APPLICANT: Old, Lloyd J.
;  TITLE OF INVENTION: Cancer Associated Antigens and Uses
;  TITLE OF INVENTION: Therefor
;  FILE REFERENCE: L0461/7062
;  CURRENT APPLICATION NUMBER: US/09/392,714A
;  CURRENT FILING DATE: 1999-09-09
;  EARLIER APPLICATION NUMBER: PCT/US98/14679
;  EARLIER FILING DATE: 1998-07-15
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-392-714-25

  Query Match             100.0%;  Score 55;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db         53 ASGPGGGAPR 62
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RESULT 5
US-09-165-546D-15
; Sequence 15, Application US/09165546D
; Patent No. 6723832
;   GENERAL INFORMATION:
;        APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
;                   Gure, Ali, Old, Lloyd, Ritter, Gerd
;        TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                            SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
;                            USES THEREOF
;        NUMBER OF SEQUENCES: 15
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FULBRIGHT & JAWORSKI LLP
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10158
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/165,546D
;             FILING DATE: 02-Oct-1998
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: April 17, 1998
;             APPLICATION NUMBER: 08/937,263
;             FILING DATE: September 15, 1997
;             APPLICATION NUMBER: US 08/725,182
;             FILING DATE: October 3, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, No. 6723832man D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3000
;             TELEFAX: (212) 318-3400
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 180 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15

  Query Match             100.0%;  Score 55;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db         53 ASGPGGGAPR 62


RESULT 6
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-9

  Query Match             100.0%;  Score 55;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db         53 ASGPGGGAPR 62


RESULT 7
US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT:  Old, Lloyd J.
;  APPLICANT:  Stockert, Elisabeth
;  APPLICANT:  Chen, Yao-Tseng
;  TITLE OF INVENTION: Colon Cancer Antigen Panel
;  FILE REFERENCE: L0461/7105(JRV)
;  CURRENT APPLICATION NUMBER: US/09/849,602
;  CURRENT FILING DATE:  2001-05-04
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-849-602-30

  Query Match             100.0%;  Score 55;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 2.7;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db         53 ASGPGGGAPR 62


RESULT 8
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL-1 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-791-495-7

  Query Match             85.5%;  Score 47;  DB 1;  Length 180;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              |||| |||||
Db         53 ASGPRGGAPR 62


RESULT 9
US-09-341-829A-7
; Sequence 7, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-7

  Query Match             85.5%;  Score 47;  DB 2;  Length 180;
  Best Local Similarity   90.0%;  Pred. No. 30;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              |||| |||||
Db         53 ASGPRGGAPR 62


RESULT 10
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL-1 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  210 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-791-495-5

  Query Match             85.5%;  Score 47;  DB 1;  Length 210;
  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              |||| |||||
Db         53 ASGPRGGAPR 62


RESULT 11
US-09-341-829A-5
; Sequence 5, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-5

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  Best Local Similarity   90.0%;  Pred. No. 34;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              |||| |||||
Db         53 ASGPRGGAPR 62


RESULT 12
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US-09-252-991A-32326
; Sequence 32326, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 32326
;   LENGTH: 421
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32326

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  Best Local Similarity   88.9%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAP 9
              | |||||||
Db        358 APGPGGGAP 366


RESULT 13
US-09-344-040C-117
; Sequence 117, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
;  APPLICANT: Tureci, Ozlem
;  APPLICANT:  Sahin, Ugur
;  APPLICANT:  Pfreundschuh, Michael
;  APPLICANT:  Ramensee, Hans Georg
;  APPLICANT:  Stevanovic, Stefan
;  TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
;  TITLE OF INVENTION:  Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
;  TITLE OF INVENTION:  Gene, and Uses Thereof
;  FILE REFERENCE: LUD 5556.1
;  CURRENT APPLICATION NUMBER: US/09/344,040C
;  CURRENT FILING DATE:  1999-06-25
;  PRIOR APPLICATION NUMBER: US 09/105,839
;  PRIOR FILING DATE: 1998-06-26
;  PRIOR APPLICATION NUMBER: US 08/851,130
;  PRIOR FILING DATE: 1997-05-05
;  NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 117
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-344-040C-117

  Query Match             78.2%;  Score 43;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGA 8
              ||||||||
Db          2 ASGPGGGA 9


RESULT 14
US-09-833-039A-117
; Sequence 117, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
;  APPLICANT: Tureci, Ozlem
;  APPLICANT:  Sahin, Ugur
;  APPLICANT:  Pfreundschuh, Michael
;  TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
;  FILE REFERENCE: LUD 5622.1
;  CURRENT APPLICATION NUMBER: US/09/833,039A
;  CURRENT FILING DATE:  2001-04-12
;  PRIOR APPLICATION NUMBER: US 09/409,455
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: US 09/344,040
;  PRIOR FILING DATE: 1999-06-26
;  PRIOR APPLICATION NUMBER: US 09/105,839
;  PRIOR FILING DATE: 1998-06-26
;  NUMBER OF SEQ ID NOS: 131
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 117
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-833-039A-117

  Query Match             78.2%;  Score 43;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGA 8
              ||||||||
Db          2 ASGPGGGA 9


RESULT 15
US-09-252-991A-24923
; Sequence 24923, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 24923
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24923

  Query Match             78.2%;  Score 43;  DB 2;  Length 210;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              | | ||||||
Db        161 ADGAGGGAPR 170


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GenCore version 5.1.7

OM protein - protein search, using sw model

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Perfect score: 55
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	100.0	10	4	US-10-447-161-39	Sequence 39, Appl
2	55	100.0	10	4	US-10-415-841A-52	Sequence 52, Appl
3	55	100.0	10	5	US-10-182-506A-23	Sequence 23, Appl
4	55	100.0	30	4	US-10-296-734-1404	Sequence 1404, Ap
5	55	100.0	179	5	US-10-482-029-202	Sequence 202, App
6	55	100.0	180	3	US-09-751-798-8	Sequence 8, Appli
7	55	100.0	180	3	US-09-849-602-30	Sequence 30, Appl
8	55	100.0	180	4	US-10-023-182-8	Sequence 8, Appli
9	55	100.0	180	4	US-10-207-655-71	Sequence 71, Appl
10	55	100.0	180	4	US-10-364-614-14	Sequence 14, Appl
11	55	100.0	180	4	US-10-026-066-3	Sequence 3, Appli
12	55	100.0	180	4	US-10-117-937-74	Sequence 74, Appl
13	55	100.0	180	4	US-10-295-027-386	Sequence 386, App
14	55	100.0	180	4	US-10-296-734-832	Sequence 832, App
15	55	100.0	180	4	US-10-188-832-139	Sequence 139, App
16	55	100.0	180	4	US-10-777-053-11	Sequence 11, Appl
17	55	100.0	180	4	US-10-751-088-15	Sequence 15, Appl
18	55	100.0	180	4	US-10-657-022-74	Sequence 74, Appl
19	55	100.0	180	4	US-10-837-217-11	Sequence 11, Appl
20	55	100.0	180	5	US-10-877-373-9	Sequence 9, Appli
21	55	100.0	180	5	US-10-723-860-1270	Sequence 1270, Ap
22	55	100.0	180	5	US-10-871-708-7	Sequence 7, Appli
23	55	100.0	180	5	US-10-895-523-3	Sequence 3, Appli
24	55	100.0	180	5	US-10-182-506A-3	Sequence 3, Appli
25	55	100.0	180	5	US-10-756-149-5024	Sequence 5024, Ap
26	55	100.0	180	6	US-11-067-064-74	Sequence 74, Appl
27	55	100.0	180	6	US-11-067-159-74	Sequence 74, Appl
28	55	100.0	397	3	US-09-821-883-27	Sequence 27, Appl
29	55	100.0	397	6	US-11-144-912-27	Sequence 27, Appl
30	55	100.0	3541	4	US-10-296-734-1454	Sequence 1454, Ap
31	47	85.5	30	4	US-10-296-734-1436	Sequence 1436, Ap
32	47	85.5	135	4	US-10-295-027-388	Sequence 388, App
33	47	85.5	135	4	US-10-188-832-141	Sequence 141, App
34	47	85.5	180	4	US-10-146-473-69	Sequence 69, Appl
35	47	85.5	180	4	US-10-117-937-75	Sequence 75, Appl
36	47	85.5	180	4	US-10-296-734-834	Sequence 834, App
37	47	85.5	180	4	US-10-468-406-4	Sequence 4, Appli
38	47	85.5	180	4	US-10-657-022-75	Sequence 75, Appl
39	47	85.5	180	5	US-10-877-373-7	Sequence 7, Appli
40	47	85.5	180	6	US-11-067-064-75	Sequence 75, Appl
41	47	85.5	180	6	US-11-067-159-75	Sequence 75, Appl
42	47	85.5	210	4	US-10-157-031-88	Sequence 88, Appl
43	47	85.5	210	4	US-10-117-937-76	Sequence 76, Appl
44	47	85.5	210	4	US-10-657-022-76	Sequence 76, Appl
45	47	85.5	210	5	US-10-877-373-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-447-161-39
; Sequence 39, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-39

Query Match 100.0%; Score 55; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
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Db 1 ASGPGGGAPR 10

RESULT 2
US-10-415-841A-52
; Sequence 52, Application US/10415841A
; Publication No. US20040131598A1
; GENERAL INFORMATION:
; APPLICANT: Tafuro, Sabrina
; APPLICANT: Meier, Ute-Christiane
; APPLICANT: McMichael, Andrew James
; APPLICANT: Bell, John Irving
; APPLICANT: Layton, Guy
; APPLICANT: Hunter, Michael
; TITLE OF INVENTION: Cancer Therapy
; FILE REFERENCE: 3547.1001-000
; CURRENT APPLICATION NUMBER: US/10/415,841A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: PCT/GB01/04844
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 52
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-841A-52

Query Match 100.0%; Score 55; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
||||||||||
Db 1 ASGPGGGAPR 10

RESULT 3
US-10-182-506A-23
; Sequence 23, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; TITLE OF INVENTION: ANTIGEN, NY ESO-1
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-23

Query Match 100.0%; Score 55; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
||||||||||
Db 1 ASGPGGGAPR 10

RESULT 4
US-10-296-734-1404
; Sequence 1404, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1404
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSO1a segment 4
US-10-296-734-1404

Query Match 100.0%; Score 55; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
||||||||||
Db 10 ASGPGGGAPR 19

RESULT 5
US-10-482-029-202
; Sequence 202, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-202

Query Match 100.0%; Score 55; DB 5; Length 179;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
||||||||||
Db 53 ASGPGGGAPR 62

RESULT 6
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. US20020010321A1
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. US20020010321A1man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3168
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-09-751-798-8

  Query Match             100.0%;  Score 55;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 7.9;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db         53 ASGPGGGAPR 62


RESULT 7
US-09-849-602-30
; Sequence 30, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT:  Old, Lloyd J.
;  APPLICANT:  Stockert, Elisabeth
;  APPLICANT:  Chen, Yao-Tseng
;  TITLE OF INVENTION: Colon Cancer Antigen Panel
;  FILE REFERENCE: L0461/7105(JRV)
;  CURRENT APPLICATION NUMBER: US/09/849,602
;  CURRENT FILING DATE:  2001-05-04
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-849-602-30

  Query Match             100.0%;  Score 55;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 7.9;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db         53 ASGPGGGAPR 62


RESULT 8
US-10-023-182-8
; Sequence 8, Application US/10023182
; Publication No. US20020164665A1
;   GENERAL INFORMATION:
;        APPLICANT: Stockert, Elisabeth; Jager, Elke;
;                   Chen, Yao-tseng; Scanlan, Matthew;
;                   Knuth, Alexander; Old, Lloyd J.
;        TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
;                            Associated Proteins, Uses Thereof,
;                            Truncated Forms of NY-ESO-1, and HLA
;                            Binding Peptides Derived Therefrom
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fulbright & Jaworski, L.L.P.
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10103
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: WordPerfect
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/023,182
;             FILING DATE: 17-Dec-2001
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/751,798
;             FILING DATE: December 29, 2000
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/725,182
;             FILING DATE: October 3, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, No. US20020164665A1man D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 5466.3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3168
;             TELEFAX: (212) 752-5958
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 180
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-023-182-8

  Query Match             100.0%;  Score 55;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 7.9;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db         53 ASGPGGGAPR 62


RESULT 9
US-10-207-655-71
; Sequence 71, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-207-655-71

  Query Match             100.0%;  Score 55;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 7.9;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db         53 ASGPGGGAPR 62


RESULT 10
US-10-364-614-14
; Sequence 14, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
;  APPLICANT: JAGER, Elke
```

```
;  APPLICANT:  KNUTH, Alexander
;  APPLICANT:  OLD, Lloyd
;  APPLICANT:  Gnjatic, Sacha
;  TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
;  FILE REFERENCE: LUD 5726.1 CIP
;  CURRENT APPLICATION NUMBER: US/10/364,614
;  CURRENT FILING DATE:  2003-02-24
;  PRIOR APPLICATION NUMBER: US 60/355,828
;  PRIOR FILING DATE: 2002-02-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-364-614-14

  Query Match             100.0%;  Score 55;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 7.9;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db         53 ASGPGGGAPR 62


RESULT 11
US-10-026-066-3
; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
; GENERAL INFORMATION:
;  APPLICANT: Simard, John J. L.
;  APPLICANT:  Diamond, David C.
;  TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
;  TITLE OF INVENTION:  PRESENTING CELLS
;  FILE REFERENCE: CTLIMM.21CP1C
;  CURRENT APPLICATION NUMBER: US/10/026,066
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: 09/561,074
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 09/560,465
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 09/561,572
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 09/561,571
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: PCT/US01/13806
;  PRIOR FILING DATE: 2001-04-27
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-026-066-3

  Query Match             100.0%;  Score 55;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 7.9;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db         53 ASGPGGGAPR 62


RESULT 12
US-10-117-937-74
; Sequence 74, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
;  APPLICANT: CTL IMMUNO THERAPIES CORP.
;  APPLICANT:  SIMARD, John, J.L.
;  APPLICANT:  DIAMOND, David, C.
;  APPLICANT:  LIU, Liping
;  APPLICANT:  XIE, Zhidong
;  TITLE OF INVENTION: EPITOPE SEQUENCES
;  FILE REFERENCE: CTLIMM.027A
;  CURRENT APPLICATION NUMBER: US/10/117,937
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: US 60/282,211
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/337,017
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: US 60/363,210
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 602
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-117-937-74

  Query Match             100.0%;  Score 55;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 7.9;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db         53 ASGPGGGAPR 62


RESULT 13
US-10-295-027-386
; Sequence 386, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Ginsberg, Wendy M.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Glynne, Richard
;  APPLICANT:  Hevezi, Peter A.
;  APPLICANT:  Mack, David H.
;  APPLICANT:  Murray, Richard
;  APPLICANT:  Watson, Susan R.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;  TITLE OF INVENTION:  Methods of Screening for Modulators of Cancer
;  FILE REFERENCE: 018501-012500US
;  CURRENT APPLICATION NUMBER: US/10/295,027
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: US 09/663,733
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/335,394
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/332,464
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: US 60/334,393
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: US 60/340,376
;  PRIOR FILING DATE: 2001-12-14
;  PRIOR APPLICATION NUMBER: US 60/347,211
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: US 60/347,349
;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: US 60/355,250
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/356,714
;  PRIOR FILING DATE: 2002-02-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1386
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 386
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; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-386

Query Match 100.0%; Score 55; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
||||||||||
Db 53 ASGPGGGAPR 62

RESULT 14
US-10-296-734-832
; Sequence 832, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 832
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYNSO1a consensus polypeptide
US-10-296-734-832

Query Match 100.0%; Score 55; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
||||||||||
Db 53 ASGPGGGAPR 62

RESULT 15
US-10-188-832-139
; Sequence 139, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-139

Query Match 100.0%; Score 55; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
||||||||||
Db 53 ASGPGGGAPR 62

Search completed: March 13, 2006, 20:02:26
Job time : 60.4706 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:54:06 ; Search time 6.82353 Seconds
(without alignments)
40.793 Million cell updates/sec

Title: US-09-529-206E-25
Perfect score: 55
Sequence: 1 ASGPGGGAPR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	100.0	180	7	US-11-155-288-7	Sequence 7, Appli
2	55	100.0	240	7	US-11-021-441-28	Sequence 28, Appl
3	43	78.2	20	6	US-10-623-155-496	Sequence 496, App
4	41	74.5	555	7	US-11-072-512-3369	Sequence 3369, Ap
5	41	74.5	953	7	US-11-037-243-66	Sequence 66, Appl
6	40	72.7	678	7	US-11-072-512-3295	Sequence 3295, Ap
7	40	72.7	1832	7	US-11-087-099-7762	Sequence 7762, Ap
8	39	70.9	213	7	US-11-072-512-2722	Sequence 2722, Ap
9	39	70.9	233	7	US-11-240-769-58	Sequence 58, Appl
10	39	70.9	430	6	US-10-992-577-8	Sequence 8, Appli
11	39	70.9	430	6	US-10-508-892-2	Sequence 2, Appli
12	39	70.9	430	7	US-11-223-294-54	Sequence 54, Appl
13	39	70.9	618	7	US-11-078-735-18	Sequence 18, Appl
14	39	70.9	618	7	US-11-050-346-63	Sequence 63, Appl
15	39	70.9	618	7	US-11-103-077-18	Sequence 18, Appl
16	39	70.9	662	7	US-11-072-175-184	Sequence 184, App
17	38	69.1	228	7	US-11-096-568A-16457	Sequence 16457, A
18	38	69.1	236	7	US-11-096-568A-22845	Sequence 22845, A
19	38	69.1	274	7	US-11-096-568A-22603	Sequence 22603, A
20	38	69.1	306	7	US-11-096-568A-20556	Sequence 20556, A
21	38	69.1	320	7	US-11-096-568A-988	Sequence 988, App
22	38	69.1	438	6	US-10-650-326B-9	Sequence 9, Appli
23	38	69.1	459	7	US-11-096-568A-21887	Sequence 21887, A
24	37	67.3	134	7	US-11-096-568A-23806	Sequence 23806, A
25	37	67.3	189	7	US-11-107-029-4	Sequence 4, Appli
26	37	67.3	198	7	US-11-096-568A-22494	Sequence 22494, A
27	37	67.3	269	7	US-11-096-568A-22493	Sequence 22493, A
28	37	67.3	379	7	US-11-109-156-16	Sequence 16, Appl
29	37	67.3	401	7	US-11-096-568A-382	Sequence 382, App
30	37	67.3	401	7	US-11-096-568A-383	Sequence 383, App
31	37	67.3	410	7	US-11-096-568A-381	Sequence 381, App
32	37	67.3	1465	7	US-11-087-099-1792	Sequence 1792, Ap
33	37	67.3	1465	7	US-11-087-099-10059	Sequence 10059, A
34	37	67.3	2923	7	US-11-200-822-3	Sequence 3, Appli
35	36.5	66.4	167	7	US-11-096-568A-10542	Sequence 10542, A
36	36.5	66.4	193	7	US-11-096-568A-21910	Sequence 21910, A
37	36.5	66.4	280	7	US-11-143-980-34	Sequence 34, Appl
38	36	65.5	55	7	US-11-114-325-14	Sequence 14, Appl
39	36	65.5	60	7	US-11-114-325-15	Sequence 15, Appl
40	36	65.5	107	7	US-11-145-861-3	Sequence 3, Appli
41	36	65.5	155	7	US-11-096-568A-19104	Sequence 19104, A
42	36	65.5	188	6	US-10-821-234-941	Sequence 941, App
43	36	65.5	237	7	US-11-096-568A-10553	Sequence 10553, A
44	36	65.5	238	7	US-11-194-890-12	Sequence 12, Appl
45	36	65.5	246	7	US-11-087-099-6549	Sequence 6549, Ap

ALIGNMENTS

RESULT 1
US-11-155-288-7
; Sequence 7, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-7

Query Match 100.0%; Score 55; DB 7; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
||||||||||
Db 53 ASGPGGGAPR 62

RESULT 2
US-11-021-441-28
; Sequence 28, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06

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;  PRIOR APPLICATION NUMBER: US 60/615,287
;  PRIOR FILING DATE: 2004-10-01
;  PRIOR APPLICATION NUMBER: US 60/599,377
;  PRIOR FILING DATE: 2004-08-05
;  PRIOR APPLICATION NUMBER: PCT/US2004/23881
;  PRIOR FILING DATE: 2004-07-23
;  PRIOR APPLICATION NUMBER: US 10/883,599
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: US 60/556,744
;  PRIOR FILING DATE: 2004-03-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion protein
US-11-021-441-28

  Query Match             100.0%;  Score 55;  DB 7;  Length 240;
  Best Local Similarity   100.0%;  Pred. No. 0.46;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAPR 10
              ||||||||||
Db        113 ASGPGGGAPR 122


RESULT 3
US-10-623-155-496
; Sequence 496, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Peckham, David W.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C20
;  CURRENT APPLICATION NUMBER: US/10/623,155
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 496
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-623-155-496

  Query Match             78.2%;  Score 43;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGA 8
              ||||||||
Db         13 ASGPGGGA 20


RESULT 4
US-11-072-512-3369
; Sequence 3369, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
;  APPLICANT: ISOGAI, TAKAO
;  APPLICANT:  SUGIYAMA, TOMOYASU
;  APPLICANT:  OTSUKI, TETSUJI
;  APPLICANT:  WAKAMATSU, AI
;  APPLICANT:  SATO, HIROYUKI
;  APPLICANT:  ISHII, SHIZUKO
;  APPLICANT:  YAMAMOTO, JUN-ICHI
;  APPLICANT:  ISONO, YUUKO
;  APPLICANT:  HIO, YURI
;  APPLICANT:  OTSUKA, KAORU
;  APPLICANT:  NAGAI, KEIICHI
;  APPLICANT:  IRIE, RYOTARO
;  APPLICANT:  TAMECHIKA, ICHIRO
;  APPLICANT:  SEKI, NAOHIKO
;  APPLICANT:  YOSHIKAWA, TSUTOMU
;  APPLICANT:  OTSUKA, MOTOYUKI
;  APPLICANT:  NAGAHARI, KENJI
;  APPLICANT:  MASUHO, YASUHIKO
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: 084335-0191
;  CURRENT APPLICATION NUMBER: US/11/072,512
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: US 60/350,978
;  PRIOR FILING DATE: 2002-01-25
;  PRIOR APPLICATION NUMBER: JP 2001-379298
;  PRIOR FILING DATE: 2001-11-05
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3369
;   LENGTH: 555
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-072-512-3369

  Query Match             74.5%;  Score 41;  DB 7;  Length 555;
  Best Local Similarity   77.8%;  Pred. No. 76;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ASGPGGGAP 9
              ||||| |:|
Db        473 ASGPGSGSP 481


RESULT 5
US-11-037-243-66
; Sequence 66, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY
;  APPLICANT:  WHYTE, DAVID
;  APPLICANT:  CAENEPEEL, SEAN
;  APPLICANT:  CHARYDCZAK, GLEN
;  APPLICANT:  MANNING, GERARD
;  APPLICANT:  SUDARSANAM, SUCHA
;  TITLE OF INVENTION: NOVEL PROTEASES
;  FILE REFERENCE: 038602/1214
;  CURRENT APPLICATION NUMBER: US/11/037,243
;  CURRENT FILING DATE:  2005-05-26
;  PRIOR APPLICATION NUMBER: US/09/888,615
;  PRIOR FILING DATE: 2001-06-26
;  PRIOR APPLICATION NUMBER: 60/214,047
;  PRIOR FILING DATE: 2000-06-26
;  NUMBER OF SEQ ID NOS: 150
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
;   LENGTH: 953
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-037-243-66

  Query Match             74.5%;  Score 41;  DB 7;  Length 953;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GPGGGAPR 10
              ||||| ||
Db        214 GPGGGHPR 221


RESULT 6
US-11-072-512-3295
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; Sequence 3295, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3295
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3295

Query Match 72.7%; Score 40; DB 7; Length 678;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASGPGGGAP 9
|:|||| |
Db 593 AAGPGGGWP 601

RESULT 7
US-11-087-099-7762
; Sequence 7762, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7762
; LENGTH: 1832
; TYPE: PRT
; ORGANISM: Podospora anserina
US-11-087-099-7762

Query Match 72.7%; Score 40; DB 7; Length 1832;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SGPGGGAPR 10
|| |||:||
Db 1051 SGSGGGSPR 1059

RESULT 8
US-11-072-512-2722
; Sequence 2722, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2722
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2722

Query Match 70.9%; Score 39; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SGPGGGA 8
|||||||
Db 56 SGPGGGA 62

RESULT 9
US-11-240-769-58
; Sequence 58, Application US/11240769
; Publication No. US20060036089A1
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: 33 Human Secreted Proteins
; FILE REFERENCE: PZ037P1C2
; CURRENT APPLICATION NUMBER: US/11/240,769
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: 09/997,131
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/628,508
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: PCT/US00/03062
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/119,468
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE

; LOCATION: (168)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-11-240-769-58

  Query Match 70.9%; Score 39; DB 7; Length 233;
  Best Local Similarity 87.5%; Pred. No. 68;
  Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GPGGGAPR 10
  ||| ||||
Db 40 GPGPGAPR 47

RESULT 10
US-10-992-577-8
; Sequence 8, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 57155-D/JPW
; CURRENT APPLICATION NUMBER: US/10/992,577
; CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-992-577-8

  Query Match 70.9%; Score 39; DB 6; Length 430;
  Best Local Similarity 77.8%; Pred. No. 1.1e+02;
  Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SGPGGGAPR 10
  ||| ||||
Db 387 SGPSSGAPR 395

RESULT 11
US-10-508-892-2
; Sequence 2, Application US/10508892
; Publication No. US20060014218A1
; GENERAL INFORMATION:
; APPLICANT: Golz, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Weingartner, Bernhard
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
; TITLE OF INVENTION: Neuropeptide FF Receptor 1 (NPFF1)
; FILE REFERENCE: Le A 35 944
; CURRENT APPLICATION NUMBER: US/10/508,892
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: PCT/EP03/02685
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: EP 02006654.4
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-508-892-2

  Query Match 70.9%; Score 39; DB 6; Length 430;
  Best Local Similarity 77.8%; Pred. No. 1.1e+02;
  Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SGPGGGAPR 10
  ||| ||||
Db 387 SGPSSGAPR 395

RESULT 12
US-11-223-294-54
; Sequence 54, Application US/11223294
; Publication No. US20060035332A1
; GENERAL INFORMATION:
; APPLICANT: HINUMA, Shuji
; APPLICANT: YOSHIDA, Hiromi
; APPLICANT: HABATA, Yugo
; APPLICANT: HOSOYA, Masaki
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: Novel RFRP-3 And Its DNA
; FILE REFERENCE: 2944US0P
; CURRENT APPLICATION NUMBER: US/11/223,294
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: US/10/487,634
; PRIOR FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: PCT/JP02/08466
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: JP 2001-254826
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 54
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Human
US-11-223-294-54

  Query Match 70.9%; Score 39; DB 7; Length 430;
  Best Local Similarity 77.8%; Pred. No. 1.1e+02;
  Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SGPGGGAPR 10
  ||| ||||
Db 387 SGPSSGAPR 395

RESULT 13
US-11-078-735-18
; Sequence 18, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137

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;  PRIOR FILING DATE: 2002-11-13
;  PRIOR APPLICATION NUMBER: PCT/GB02/05133
;  PRIOR FILING DATE: 2002-11-13
;  PRIOR APPLICATION NUMBER: GB 0220912.0
;  PRIOR FILING DATE: 2002-09-10
;  PRIOR APPLICATION NUMBER: GB 0220913.8
;  PRIOR FILING DATE: 2002-09-10
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 18
;   LENGTH: 618
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-078-735-18

  Query Match             70.9%;  Score 39;  DB 7;  Length 618;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GPGGGAPR 10
              ||| ||||
Db         40 GPGPGAPR 47


RESULT 14
US-11-050-346-63
; Sequence 63, Application US/11050346
; Publication No. US20060002924A1
; GENERAL INFORMATION:
;  APPLICANT: BODMER, MARK WILLIAM
;  APPLICANT:  CHAMPION, BRIAN ROBERT
;  APPLICANT:  LENNARD, ANDREW CHRISTOPHER
;  APPLICANT:  MCKENZIE, GRAHAME JAMES
;  APPLICANT:  TUGAL, TAMARA
;  APPLICANT:  WARD, GEORGE ALBERT
;  TITLE OF INVENTION: CONJUGATE OF NOTCH SIGNALLING PATHWAY MODULATORS AND
;  TITLE OF INVENTION:  THEIR USE IN MEDICAL TREATMENT
;  FILE REFERENCE: 674525-2016
;  CURRENT APPLICATION NUMBER: US/11/050,346
;  CURRENT FILING DATE:  2005-02-03
;  PRIOR APPLICATION NUMBER: GB 0312062.3
;  PRIOR FILING DATE: 2003-05-24
;  PRIOR APPLICATION NUMBER: PCT/GB03/01525
;  PRIOR FILING DATE: 2003-04-04
;  PRIOR APPLICATION NUMBER: GB 0300234.2
;  PRIOR FILING DATE: 2003-01-07
;  PRIOR APPLICATION NUMBER: GB 0218068.5
;  PRIOR FILING DATE: 2002-08-03
;  PRIOR APPLICATION NUMBER: GB 0220849.4
;  PRIOR FILING DATE: 2002-09-07
;  PRIOR APPLICATION NUMBER: GB 0220912.0
;  PRIOR FILING DATE: 2002-09-10
;  PRIOR APPLICATION NUMBER: GB 0220913.8
;  PRIOR FILING DATE: 2002-09-10
;  PRIOR APPLICATION NUMBER: PCT/GB02/05137
;  PRIOR FILING DATE: 2002-11-13
;  PRIOR APPLICATION NUMBER: PCT/GB02/05133
;  PRIOR FILING DATE: 2002-11-13
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 63
;   LENGTH: 618
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-050-346-63

  Query Match             70.9%;  Score 39;  DB 7;  Length 618;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GPGGGAPR 10
              ||| ||||
Db         40 GPGPGAPR 47


RESULT 15
US-11-103-077-18
; Sequence 18, Application US/11103077
; Publication No. US20060003927A1
; GENERAL INFORMATION:
;  APPLICANT: CHAMPION, BRIAN ROBERT
;  APPLICANT:  YOUNG, LESLEY LYNN
;  TITLE OF INVENTION: MODULATION OF IMMUNE FUNCTION
;  FILE REFERENCE: 674525-2020
;  CURRENT APPLICATION NUMBER: US/11/103,077
;  CURRENT FILING DATE:  2005-04-11
;  PRIOR APPLICATION NUMBER: PCT/GB03/04402
;  PRIOR FILING DATE: 2003-10-09
;  PRIOR APPLICATION NUMBER: GB 0223405.2
;  PRIOR FILING DATE: 2002-10-09
;  PRIOR APPLICATION NUMBER: GB 0223409.4
;  PRIOR FILING DATE: 2002-10-09
;  PRIOR APPLICATION NUMBER: GB 0224353.3
;  PRIOR FILING DATE: 2002-10-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 18
;   LENGTH: 618
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-103-077-18

  Query Match             70.9%;  Score 39;  DB 7;  Length 618;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 GPGGGAPR 10
              ||| ||||
Db         40 GPGPGAPR 47


Search completed: March 13, 2006, 20:03:30
Job time : 7.82353 secs
```

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 18:52:59 ; Search time 112.941 Seconds
(without alignments)
58.355 Million cell updates/sec

Title: US-09-529-206E-26
Perfect score: 78
Sequence: 1 AGAARASGPGGGAPR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	78	100.0	15	2	AAY05978	Aay05978 Human can
2	78	100.0	20	2	AAY05979	Aay05979 Human can
3	78	100.0	30	5	AAU85105	Aau85105 Human NYN
4	78	100.0	179	8	ADK68648	Adk68648 Epitope 1
5	78	100.0	180	2	AAW62584	Aaw62584 Cancer as
6	78	100.0	180	2	AAW69665	Aaw69665 Human NY-
7	78	100.0	180	2	AAY05965	Aay05965 Human can
8	78	100.0	180	3	AAY52430	Aay52430 Human tum
9	78	100.0	180	3	AAY70862	Aay70862 Human tum
10	78	100.0	180	3	AAB03154	Aab03154 Human oes
11	78	100.0	180	4	AAB69946	Aab69946 Human NY-
12	78	100.0	180	4	AAG67164	Aag67164 Amino aci
13	78	100.0	180	4	AAU01535	Aau01535 Human NY-
14	78	100.0	180	4	AAE07714	Aae07714 Human NY
15	78	100.0	180	5	AAU84818	Aau84818 Human NYN
16	78	100.0	180	5	AAU11543	Aau11543 Human tum
17	78	100.0	180	6	ABR58672	Abr58672 Human can
18	78	100.0	180	6	ABR48210	Abr48210 Human bla
19	78	100.0	180	6	ABU56508	Abu56508 Lung canc
20	78	100.0	180	6	ABU56694	Abu56694 Lung canc
21	78	100.0	180	6	ABP74198	Abp74198 Human NY-
22	78	100.0	180	6	ABU64816	Abu64816 Human NY-
23	78	100.0	180	6	ABR83438	Abr83438 Human NY-
24	78	100.0	180	7	ADC09576	Adc09576 NY-ESO-1
25	78	100.0	180	7	ADD35564	Add35564 Human NY-
26	78	100.0	180	7	ADD35568	Add35568 Human NY-
27	78	100.0	180	7	ADD25510	Add25510 Binding d
28	78	100.0	180	7	ADN39068	Adn39068 Cancer/an
29	78	100.0	180	8	ADJ54139	Adj54139 Human NY-
30	78	100.0	180	8	ADM72815	Adm72815 Human NY-
31	78	100.0	180	8	ADM73418	Adm73418 CAG-3 pro
32	78	100.0	180	8	ADM73417	Adm73417 Human NY-
33	78	100.0	180	8	ADQ18451	Adq18451 Human sof
34	78	100.0	180	8	ADQ10446	Adq10446 Autoimmun
35	78	100.0	180	8	ADS80926	Ads80926 Tumour as
36	78	100.0	180	9	ADW44353	Adw44353 Human aut
37	78	100.0	180	9	ADY85096	Ady85096 Tumor ant
38	78	100.0	180	9	ADZ28913	Adz28913 NY-ESO-1
39	78	100.0	180	9	ADZ42374	Adz42374 Immunogen
40	78	100.0	180	9	AEA35651	Aea35651 Human NY-
41	78	100.0	240	9	ADW99402	Adw99402 NY-ESO-1/
42	78	100.0	240	9	AEB80047	Aeb80047 Human NY-
43	78	100.0	397	4	AAE13122	Aae13122 NY-ESO-IC
44	78	100.0	3541	5	AAU85130	Aau85130 Human mel
45	74	94.9	14	2	AAY05986	Aay05986 Human can

ALIGNMENTS

RESULT 1
AAY05978
ID AAY05978 standard; peptide; 15 AA.
XX
AC AAY05978;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Claim 15; Page 64; 88pp; English.
XX
CC The present sequence represents a cancer peptide that corresponds to
CC amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
CC AAY05965), a new and potent tumour antigen capable of eliciting an
CC antigen specific immune response by T cells. Cancer peptides derived from
CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
CC variants (see AAY05967-87), are useful as cancer vaccines that protect
CC against cancer. The invention provides: vectors and host cells (also
CC useful as vaccines); a method of diagnosis of cancer or precancer; a
CC transgenic animal; antisense oligonucleotides that inhibit expression of

CC the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
CC cancer peptide, useful in diagnostic and detection assays; and methods
CC for preventing or inhibiting cancer by administering a cancer peptide,
CC with or without an HLA molecule. The cancer peptides form part of, or are
CC derived from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
CC treated by inducing cancer-specific T cells in vitro for subsequent
CC return to a patient
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 78; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAPR 15
||||||||||||||||
Db 1 AGAARASGPGGGAPR 15

RESULT 2
AAY05979
ID AAY05979 standard; peptide; 20 AA.
XX
AC AAY05979;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Claim 16; Page 64; 88pp; English.
XX
CC The present sequence represents a cancer peptide that is based on amino
CC acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965),
CC a new and potent tumour antigen capable of eliciting an antigen specific
CC immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-
CC 3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-
CC 87), are useful as cancer vaccines that protect against cancer. The
CC invention provides: vectors and host cells (also useful as vaccines); a
CC method of diagnosis of cancer or precancer; a transgenic animal;
CC antisense oligonucleotides that inhibit expression of the cancer peptide
CC or tumour antigen; antibodies reacting with a CAG-3 cancer peptide,
CC useful in diagnostic and detection assays; and methods for preventing or
CC inhibiting cancer by administering a cancer peptide, with or without an
CC HLA molecule. The cancer peptides form part of, or are derived from,
CC cancers such as primary or metastatic melanoma, thymoma, lymphoma,
CC sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
CC cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
CC prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by
CC inducing cancer-specific T cells in vitro for subsequent return to a
CC patient
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 78; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAPR 15
||||||||||||||||
Db 6 AGAARASGPGGGAPR 20

RESULT 3
AAU85105
ID AAU85105 standard; peptide; 30 AA.
XX
AC AAU85105;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human NYNSO1a segment 4.
XX
KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW viral infection; human immunodeficieny virus; melanoma;
KW bacterial infection; Salmonella; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
XX
OS Homo sapiens.
XX
PN WO200190197-A1.
XX
PD 29-NOV-2001.
XX
PF 25-MAY-2001; 2001WO-AU000622.
XX
PR 26-MAY-2000; 2000AU-00007761.
XX
PA (AUSU) UNIV AUSTRALIAN NAT.
XX
PI Thomson SA, Ramshaw IA;
XX
DR WPI; 2002-147575/19.
DR N-PSDB; ABK36925.
XX
PT New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
PS Example 3; Fig 27; 364pp; English.
XX
CC The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human

CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention
XX
SQ Sequence 30 AA;

Query Match 100.0%; Score 78; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAPR 15
||||||||||||||||
Db 5 AGAARASGPGGGAPR 19

RESULT 4
ADK68648
ID ADK68648 standard; protein; 179 AA.
XX
AC ADK68648;
XX
DT 06-MAY-2004 (first entry)
XX
DE Epitope liberation-related NY-ESO-1 protein SeqID11.
XX
KW epitope liberation; substrate; proteasome; cytostatic; antibacterial;
KW protozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope;
KW cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;
KW virus; bacterium; protozoan; fungus; housekeeping proteasome system;
KW human.
XX
OS Homo sapiens.
XX
PN US2003228634-A1.
XX
PD 11-DEC-2003.
XX
PF 07-NOV-2002; 2002US-00292413.
XX
PR 07-NOV-2001; 2001US-0336968P.
XX
PA (SIMA/) SIMARD J J L.
PA (DIAM/) DIAMOND D C.
PA (QIUZ/) QIU Z.
PA (LEIX/) LEI X.
XX
PI Simard JJL, Diamond DC, Qiu Z, Lei X;
XX
DR WPI; 2004-167209/16.
DR N-PSDB; ADK68674.
XX
PT Identifying polypeptide suitable for epitope e.g., housekeeping epitope,
PT liberation by contacting substrate polypeptide comprising epitope of
PT interest, with proteasome, and assaying for liberation of epitope.
XX
PS Example 2; SEQ ID NO 11; 67pp; English.
XX
CC This invention relates to a novel method of identifying a polypeptide
CC suitable for epitope liberation, including the steps of identifying an
CC epitope of interest; providing substrate polypeptide sequence including
CC the epitope, wherein the substrate permits processing by a proteasome;
CC contacting the substrate with a composition including the proteasome,
CC under conditions that support processing of the substrate by proteasome;
CC and assaying for liberation of epitope. The invention may be useful for
CC the development of compounds with a cytostatic, antibacterial,
CC protozoacide or fungicide activity acting as T-cell activators. In
CC addition, the invention may allow development of a vaccine. The invention
CC is useful for identifying a polypeptide suitable for epitope liberation,
CC where the epitope is a housekeeping epitope. The compositions comprising
CC the identified housekeeping epitopes are useful in vitro in vaccine
CC development or in the generation or expansion of cytotoxic T lymphocyte
CC (CTL) to be used in adoptive immunotherapy. The invention is also useful
CC for activating T-cells against neoplastic cells, and cells infected with
CC virus, bacterium, protozoan or fungus. CTL epitopes are identified based
CC on the knowledge that such epitopes are, in fact, produced by the
CC housekeeping proteasome system. Once identified, these epitopes, embodied
CC as peptides, can be used to successfully immunise or induce therapeutic
CC CTL responses against housekeeping proteasome expressing target cells in
CC the host. The present sequence is that of a protein which is related to
CC the method of the invention.
XX
SQ Sequence 179 AA;

Query Match 100.0%; Score 78; DB 8; Length 179;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAPR 15
||||||||||||||||
Db 47 AGAARASGPGGGAPR 61

RESULT 5
AAW62584
ID AAW62584 standard; protein; 180 AA.
XX
AC AAW62584;
XX
DT 17-SEP-1998 (first entry)
XX
DE Cancer associated antigen NY-ESO-1.
XX
KW Cancer associated antigen; NY-ESO-1; regression; progression; onset;
KW cancer; treatment; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 7
FT /note= "potential myristorylation site"
FT Misc-difference 9
FT /note= "potential myristorylation site"
FT Misc-difference 11
FT /note= "potential phosphorylation site"
FT Misc-difference 98
FT /note= "potential phosphorylation site"
FT Misc-difference 134
FT /note= "potential phosphorylation site"
FT Misc-difference 138
FT /note= "potential phosphorylation site"
XX
PN WO9814464-A1.
XX
PD 09-APR-1998.
XX
PF 15-SEP-1997; 97WO-US016335.
XX
PR 03-OCT-1996; 96US-00725182.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Chen Y, Scanlan M, Gure A, Old LJ, Jager E, Knuth A;
PI Drijfhout JW;
XX
DR WPI; 1998-286417/25.
DR N-PSDB; AAV38566.
XX
PT New isolated cancer associated antigen - is used to develop products for
PT the diagnosis and treatment of cancers and for monitoring cancer therapy.
XX
PS Claim 8; Fig 3; 49pp; English.

XX
CC The present sequence represents a cancer associated antigen. The clone
CC from which the DNA sequence is obtained is designated NY-ESO-1. The
CC specification described a method for determining regression, progression
CC of onset of a cancerous condition, comprising monitoring a sample from a
CC patient with the cancerous condition for a parameter selected from NY-ESO
CC -1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells
CC specific for the peptide and an MHC molecule with which it non-covalently
CC complexes. Methods for the treatment of a cancerous condition are also
CC described. The NY-ESO-1 protein and peptides derived from it can be used
CC for diagnosis and treatment of cancers and to monitor the efficacy of a
CC therapeutic regime
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 78; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAPR 15
||||||||||||||||
Db 48 AGAARASGPGGGAPR 62

RESULT 6
AAW69665
ID AAW69665 standard; protein; 180 AA.
XX
AC AAW69665;
XX
DT 27-OCT-1998 (first entry)
XX
DE Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
XX
KW Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
XX
OS Homo sapiens.
XX
PN WO9832855-A1.
XX
PD 30-JUL-1998.
XX
PF 27-JAN-1998; 98WO-US001445.
XX
PR 27-JAN-1997; 97US-00791495.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Lethe B, Lucas S, De Smet C, Godelaine D, Boon-Falleur T;
XX
DR WPI; 1998-427951/36.
DR N-PSDB; AAV50348.
XX
PT New isolated LAGE-1 tumour associated nucleic acids - used to develop
PT products for the diagnosis and treatment of LAGE-1 associated disorders,
PT particularly tumours.
XX
PS Example 2; Page 57-58; 73pp; English.
XX
CC The present sequence represents human NY-ESO-1, formerly known as LL-1.2
CC clone, which is used in an example from the present invention which
CC describes LAGE-1 tumour associated protein (TAP). The present invention
CC also describes: (1) a method for treating a subject with a disorder
CC characterised by expression of a LAGE-1 nucleic acid molecule or an
CC expression product, comprising administering to the subject autologous
CC cytolytic T cells to ameliorate the disorder, where the cytolytic T cells
CC are specific for complexes of an HLA molecule and a LAGE-1 TAP or an
CC immunogenic fragment; (2) a method for treating a subject with a disorder
CC characterised by expression of a LAGE-1 nucleic acid molecule or an
CC expression product, comprising administering a LAGE-1 TAP or an
CC immunogenic fragment to ameliorate the disorder; and (3) a method for
CC selectively enriching a population of T cells with cytolytic T cells
CC specific for a LAGE-1 TAP comprising contacting an isolated population of
CC T cells with an agent presenting a complex of a LAGE TAP or an
CC immunogenic fragment and a HLA presenting molecule to selectively enrich
CC the isolated population of T cells with the cytolytic T cells. The
CC methods and products from the present invention can be used for the
CC diagnosis and treatment of LAGE-1 associated disorders, particularly
CC tumours
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 78; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAPR 15
||||||||||||||||
Db 48 AGAARASGPGGGAPR 62

RESULT 7
AAY05965
ID AAY05965 standard; protein; 180 AA.
XX
AC AAY05965;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia;
KW non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis;
KW melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer;
KW breast cancer; prostate cancer; ovarian cancer; cervical cancer;
KW bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma;
KW tumour; diagnosis; immunotherapy; therapy; vaccine; ORF1.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
DR N-PSDB; AAX58599.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Claim 4; Fig 3A; 88pp; English.
XX
CC The present sequence represents the ORF1 protein encoded by open reading
CC frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and
CC potent tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides comprising ORF1, ORF2 (see
CC AAY05966), portions of these peptides and their variants (see AAY05965-
CC 87), are useful as cancer vaccines that protect the recipient from
CC development of cancer. The invention provides: vectors and host cells
CC (also useful as vaccines); a method of diagnosis of cancer or precancer;
CC a transgenic animal; antisense oligonucleotides that inhibit expression
CC of the cancer peptide or tumour antigen; antibodies reacting with the CAG
CC -3 cancer peptide, useful in diagnostic and detection assays; and methods
CC for preventing or inhibiting cancer by administering a cancer peptide,
CC with or without an HLA molecule. The cancer peptides form part of, or are
CC derived from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is

```
CC   treated by inducing cancer-specific T cells in vitro for subsequent
CC   return to a patient
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 78;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 8
AAY52430
ID   AAY52430 standard; protein; 180 AA.
XX
AC   AAY52430;
XX
DT   21-OCT-2004  (revised)
DT   15-FEB-2000  (first entry)
XX
DE   Human tumour antigen NY-ESO-1.
XX
KW   Cancer; tumour; antigen; MHC; major histocompatility complex; T-cell;
KW   cytotoxic; helper; stimulation; proliferation; treatment; diagnosis;
KW   prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;
KW   hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Peptide          44. .53
FT                    /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide          60. .69
FT                    /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide          60. .68
FT                    /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide          63. .72
FT                    /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide          79. .88
FT                    /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide          79. .87
FT                    /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
FT                    and HLA-B35"
FT   Peptide          82. .91
FT                    /note= "Peptide presented by MHC Class I HLA-A1"
FT   Peptide          82. .90
FT                    /note= "Peptide presented by MHC Class I HLA-A1"
FT   Peptide          83. .91
FT                    /note= "Peptide presented by MHC Class I HLA-B44"
FT   Peptide          84. .92
FT                    /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
FT                    and HLA-B35"
FT   Peptide          87. .96
FT                    /note= "Peptide presented by MHC Class I HLA-A1"
FT   Peptide          88. .96
FT                    /note= "Peptide presented by MHC Class I HLA-B44"
FT   Peptide          96. .104
FT                    /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide          100. .108
FT                    /note= "Peptide presented by MHC Class I HLA-B44"
FT   Peptide          102. .110
FT                    /note= "Peptide presented by MHC Class I HLA-B44"
FT   Peptide          107. .116
FT                    /note= "Peptide presented by MHC Class I HLA-A24"
FT   Peptide          110. .118
FT                    /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide          113. .122
FT                    /note= "Peptide presented by MHC Class I HLA-B7 and HLA-
FT                    B52"
FT   Peptide          113. .121
FT                    /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide          115. .124
FT                    /note= "Peptide presented by MHC Class I HLA-A3"
FT   Peptide          118. .126
FT                    /note= "Peptide presented by MHC Class I HLA-B35"
FT   Peptide          124. .133
FT                    /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide          125. .133
FT                    /note= "Peptide presented by MHC Class I HLA-A24"
FT   Peptide          138. .147
FT                    /note= "Peptide presented by MHC Class I HLA-B8"
FT   Peptide          139. .147
FT                    /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide          145. .153
FT                    /note= "Peptide presented by MHC Class I HLA-A24 and HLA-
FT                    B52"
FT   Peptide          153. .162
FT                    /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide          154. .163
FT                    /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide          154. .162
FT                    /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide          156. .167
FT                    /note= "Peptide (AAY52434) presented by MHC Class I HLA-
FT                    A2"
FT   Peptide          158. .166
FT                    /note= "Peptide presented by MHC Class I HLA-A3"
FT   Peptide          159. .167
FT                    /note= "Peptide presented by MHC Class I HLA-A3"
FT   Peptide          162. .170
FT                    /note= "Peptide presented by MHC Class I HLA-B52"
XX
PN   WO9953938-A1.
XX
PD   28-OCT-1999.
XX
PF   24-MAR-1999;   99WO-US006875.
XX
PR   17-APR-1998;   98US-00062422.
PR   02-OCT-1998;   98US-00165546.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Stockert E,  Jager E,  Chen Y,  Scanlan M,  Alexander K,  Old LJ;
PI   Gure A,  Ritter G;
XX
DR   WPI; 2000-038483/03.
DR   N-PSDB; AAZ38380.
XX
PT   Novel peptides which bind to MHC class I and MHC class II molecules,
PT   useful for therapeutic and diagnostic purposes.
XX
PS   Claim 30; Fig 3; 49pp; English.
XX
CC   This sequence represents a human tumour antigen, NY-ESO-1, the cDNA
CC   encoding which was isolated from an oesophagus squamous cell cancer cDNA
CC   library. Tissue localisation studies revealed it to be expressed at high
CC   levels in normal ovary and testis but not in normal colon, kidney, liver,
CC   brain, oesophagus and skin. It was expressed in certain tumours and
CC   tumour cell lines with some degree of frequency - these included melanoma
CC   specimens and cell lines, and breast and bladder cancer specimens, with
CC   expression in other tumour types being sporadic. Peptides derived from NY
CC   -ESO-1 are bound by both MHC (major histocompatibility complex) Class I
CC   and Class II molecules for presentation to T-cells. Peptides AAY52431-
CC   Y52434 bind to Class I HLA-A2 molecules, thereby stimulating
CC   proliferation of cytotoxic T-cells, while peptides AAY52435-Y52440 bind
CC   to Class II HLA-DR53 molecules, stimulating helper T-cell proliferation.
CC   The peptides derived from NY-ESO-1 may be used in methods and
CC   compositions used for the treatment, diagnosis and prevention of cancers
CC   (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma,
CC   ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to
CC   stimulate the proliferation of T cells
```

```
CC
CC   Revised record issued on 21-OCT-2004 : Correction to feature table key
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 78;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 9
AAY70862
ID   AAY70862 standard; protein; 180 AA.
XX
AC   AAY70862;
XX
DT   31-JUL-2000  (first entry)
XX
DE   Human tumour antigen, NY-ESO-1 protein.
XX
KW   NY-ESO-1; CAMEL; CTL-recognised Antigen on MELanoma; human; cancer; CTL;
KW   cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer;
KW   melanoma; immunotherapy; immune response.
XX
OS   Homo sapiens.
XX
PN   WO200023584-A1.
XX
PD   27-APR-2000.
XX
PF   15-OCT-1999;   99WO-EP007832.
XX
PR   16-OCT-1998;   98EP-00119583.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA   (UYHO-) UNIV HOSPITAL LEIDEN.
XX
PI   Schrier PI,  Aarnoudse CA,  Heider K,  Klade C;
XX
DR   WPI; 2000-339685/29.
DR   N-PSDB; AAD00152.
XX
PT   Tumor-associated antigen useful for cancer immunotherapy is encoded by
PT   the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
XX
PS   Example 3; Page 62-63; 73pp; English.
XX
CC   The present sequence is the human NY-ESO-1 protein, a tumour antigen,
CC   identified by screening an esophagus carcinoma cDNA library. This protein
CC   is derived from open reading frame (ORF)-1 that contain epitopes of
CC   tumour specific T-cells. NY-ESO-1 is expressed in different tumour types,
CC   but not in healthy tissues except in testis. It also shows homology with
CC   the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELanoma)
CC   protein, a tumour-asociated antigen. The tumour-associated antigen
CC   displayed on melanoma cells is recognised by cytotoxic T lymphocytes.
CC   This sequence has anticancer activity. CAMEL tumour antigen and
CC   immunogenic peptides derived from it are useful for cancer immunotherapy.
CC   They have the potential to induce an immune response, by eliciting a CTL
CC   response. The DNA molecule is used for the construction of recombinant or
CC   fusion proteins
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 78;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 10
AAB03154
ID   AAB03154 standard; protein; 180 AA.
XX
AC   AAB03154;
XX
DT   23-OCT-2000  (first entry)
XX
DE   Human oesophageal cancer-associated antigen NY-ESO-1.
XX
KW   Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen;
KW   oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain;
KW   antibody; diagnostic marker; drug delivery target.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   7
FT                   /note= "Potential N-myristoylation site"
FT   Modified-site   9
FT                   /note= "Potential N-myristoylation site"
FT   Modified-site   11
FT                   /note= "Potential O-phosphorylation site"
FT   Modified-site   98
FT                   /note= "Potential O-phosphorylation site"
FT   Modified-site   134
FT                   /note= "Potential O-phosphorylation site"
FT   Modified-site   138
FT                   /note= "Potential O-phosphorylation site"
FT   Domain          152. .172
FT                   /note= "Potential transmembrane domain"
XX
PN   US6069233-A.
XX
PD   30-MAY-2000.
XX
PF   26-JAN-1998;   98US-00013150.
XX
PR   03-OCT-1996;   96US-00725381.
XX
PA   (SLOK ) SLOAN KETTERING INST CANCER RES.
PA   (CORR ) CORNELL RES FOUND INC.
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Scanlan M,  Gure AO,  Chen Y,  Tureci O,  Sahin U,  Pfreundschuh M;
PI   Old LJ;
XX
DR   WPI; 2000-410880/35.
DR   N-PSDB; AAA61483.
XX
PT   New isolated esophageal cancer-associated antigen useful as markers for
PT   producing antibodies and as targets for identifying abnormal conditions,
PT   e.g. infections and cancer.
XX
PS   Example 5; Fig 3; 9pp; English.
XX
CC   This sequence represents a human oesophageal cancer-associated antigen,
CC   NY-ESO-1. The cDNA encoding this sequence was isolated from a cDNA
CC   library prepared from a specimen of well-to-moderately differentiated
CC   squamous cell cancer of the oesophagus. Expression analysis demonstrated
CC   that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma
CC   cell lines and in normal ovary and testis tissue, but not in normal
CC   colon, kidney, liver or brain tissue. Analysis of the amino acid sequence
CC   of the protein indicates that the protein has a transmembrane domain,
CC   several N-myristoylation sites and O-phosphorylation sites and that it
CC   contains antigenic sequences in the N-terminal half of the protein. The
CC   antigen is useful as an immunogen when combined with an adjuvant, in both
CC   precursor and post- translationally modified forms, and may be used to
CC   generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic
CC   marker for oesophageal cancer, and can be utilised as a marker for the
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CC   targetted delivery of therapeutic agents to oesophageal cancer cells. It
CC   can also be used to generate diagnostic or therapeutic agents
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 78;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 11
AAB69946
ID   AAB69946 standard; protein; 180 AA.
XX
AC   AAB69946;
XX
DT   27-APR-2001  (first entry)
XX
DE   Human NY-ESO-1 protein.
XX
KW   Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW   HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW   non-small cell lung carcinoma; tumour status determination.
XX
OS   Homo sapiens.
XX
PN   WO200107917-A1.
XX
PD   01-FEB-2001.
XX
PF   14-JUL-2000; 2000WO-US019220.
XX
PR   23-JUL-1999;   99US-00359503.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (SLOK ) SLOAN KETTERING INST CANCER RES.
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Jager E,  Stockert E,  Old LJ,  Knuth A,  Chen Y,  Scanlan M;
XX
DR   WPI; 2001-182822/18.
DR   N-PSDB; AAF58634.
XX
PT   Method useful for determining the status (e.g. progression, regression or
PT   stability of the disease) of a cancerous condition, involves determining
PT   the levels of NY-ESO-1 specific antibodies in a sample taken from a
PT   patient.
XX
PS   Example 5; Fig 3; 50pp; English.
XX
CC   The present sequence is human NY-ESO-1 protein. It is provided in a
CC   specification relating to a method for determining the status of a
CC   cancerous condition in a patient with a tumour that expresses NY-ESO-1.
CC   The method comprises assaying a sample taken from the patient for
CC   antibodies that specifically bind to the NY-ESO-1 and comparing the value
CC   obtained to a prior value obtained from assay of a prior sample taken
CC   from the patient. Any difference between the values is indicative of a
CC   change in status of the cancerous condition. The method is useful for
CC   determining whether a cancerous condition is progressing, regressing or
CC   remaining stable, in particular in patients receiving treatment for a
CC   melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
CC   carcinoma
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 78;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 12
AAG67164
ID   AAG67164 standard; protein; 180 AA.
XX
AC   AAG67164;
XX
DT   13-NOV-2001  (first entry)
XX
DE   Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
XX
KW   Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW   HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
KW   cancer; testis tumour.
XX
OS   Homo sapiens.
XX
PN   WO200162917-A1.
XX
PD   30-AUG-2001.
XX
PF   22-JAN-2001; 2001WO-US002126.
XX
PR   22-FEB-2000; 2000US-00510635.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Lethe B,  Boon-Falleur T;
XX
DR   WPI; 2001-550091/61.
DR   N-PSDB; AAH75118.
XX
PT   Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful
PT   for diagnosing testicular tumors.
XX
PS   Example 5; Fig 3; 50pp; English.
XX
CC   The present sequence represents cancer testis tumour antigen NY-ESO-1
CC   (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
CC   least one human leukocyte antigen (HLA) binding peptide, which binds to
CC   Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is
CC   expressed in tumour mRNA and in testis, but not normal colon, kidney,
CC   liver or brain tissue. The presence or level of expression of NY-ESO-1
CC   may be assayed for the diagnosis of cancer, especially testis tumours
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 78;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 13
AAU01535
ID   AAU01535 standard; protein; 180 AA.
XX
AC   AAU01535;
XX
DT   18-JUL-2001  (first entry)
XX
DE   Human NY-ESO-1 tumour rejection antigen precursor protein.
XX
KW   NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW   major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW   human leukocyte antigen-determining region; disease progression;
```

```
KW   disease regression; disease onset; body tissue; body fluid; enzyme label;
KW   radioactive label; monoclonal antibody.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   7
FT                   /note= "Myristoylated"
FT   Modified-site   9
FT                   /note= "Myristoylated"
FT   Modified-site   11
FT                   /note= "Phosphorylated"
FT   Modified-site   98
FT                   /note= "Phosphorylated"
FT   Modified-site   134
FT                   /note= "Phosphorylated"
FT   Modified-site   138
FT                   /note= "Phosphorylated"
XX
PN   WO200123560-A2.
XX
PD   05-APR-2001.
XX
PF   26-SEP-2000; 2000WO-US026411.
XX
PR   29-SEP-1999;   99US-00408036.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Tureci O,  Sahin U,  Pfreundschuh M;
XX
DR   WPI; 2001-266156/27.
DR   N-PSDB; AAS02254.
XX
PT   Polypeptides binding to major histocompatibility complex class II human
PT   leukocyte antigen-determining region molecule having amino acid sequence
PT   found in tumor rejection antigen precursor used for stimulating
PT   proliferation of helper T cells.
XX
PS   Claim 4; Fig 3; 62pp; English.
XX
CC   The sequence represents a human NY-ESO-1 tumour rejection antigen
CC   precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to
CC   major histocompatibility complex (MHC) Class II molecules such as human
CC   leukocyte antigen-determining region (HLA-DR) molecules and stimulate
CC   proliferation of helper T cells. The peptides can be administered to an
CC   HLA-DR positive subject in order to stimulate the helper T cells. An MHC
CC   Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell
CC   or present in free form is useful for this stimulation. The nucleic acid
CC   is useful for screening for a cancerous condition, which involves
CC   contacting a subject sample to a cell line transfected with the
CC   immunoreactive cell (helper T cell), where interaction is indicative of
CC   cancer. In addition, a sample from a patient (for example, a body fluid
CC   or tissue) can be monitored for the amount of the complex present in the
CC   bloodstream. This is useful for determining regression, progression or
CC   onset of a cancerous condition. The method involves contacting the sample
CC   with a radioactive labelled or enzyme labelled monoclonal antibody which
CC   specifically binds with the complex
XX
SQ   Sequence 180 AA;

  Query Match            100.0%;  Score 78;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 14
AAE07714
ID   AAE07714 standard; protein; 180 AA.
XX
AC   AAE07714;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human NY ESO-1 protein.
XX
KW   Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW   class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW   NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW   tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW   immunotherapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 45. .47
FT                   /note= "Encoded by CCCGGGGC"
XX
PN   WO200155393-A2.
XX
PD   02-AUG-2001.
XX
PF   26-JAN-2001; 2001WO-US002765.
XX
PR   28-JAN-2000; 2000US-0179004P.
PR   29-SEP-2000; 2000US-0237107P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang R,  Rosenberg SA,  Zeng G;
XX
DR   WPI; 2001-496851/54.
DR   N-PSDB; AAD14179, AAD14180.
XX
PT   New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT   useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT   protection from metastasis.
XX
PS   Example 1; Fig 1; 134pp; English.
XX
CC   The invention relates to the identification and isolation of major
CC   histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC   epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC   from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC   antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC   restricted. The products of the gene are promising candidates for
CC   immunotherapeutic strategies for the prevention, treatment and diagnosis
CC   of patients with cancer. The cancer epitopes are useful as immunogen and
CC   vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC   lymphocytes resulting in protection of the recipient from development of
CC   cancer and protection from metastasis, or by inhibiting the growth of
CC   cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC   useful as diagnostic agent to detect the presence of cancer, to enhance
CC   the generation of antibody and/or CD8+ T cell responses against any given
CC   target antigen and/or hapten and to induce tumour-specific humoral-
CC   mediated immunity against cancer. The present sequence is human NY ESO-1
CC   protein
XX
SQ   Sequence 180 AA;

  Query Match            100.0%;  Score 78;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 15
AAU84818
ID   AAU84818 standard; protein; 180 AA.
```

XX
AC AAU84818;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human NYNSO1a consensus sequence.
XX
KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW viral infection; human immunodeficieny virus; melanoma;
KW bacterial infection; Salmonella; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
XX
OS Homo sapiens.
XX
PN WO200190197-A1.
XX
PD 29-NOV-2001.
XX
PF 25-MAY-2001; 2001WO-AU000622.
XX
PR 26-MAY-2000; 2000AU-00007761.
XX
PA (AUSU) UNIV AUSTRALIAN NAT.
XX
PI Thomson SA, Ramshaw IA;
XX
DR WPI; 2002-147575/19.
XX
PT New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
PS Example 3; Fig 27; 364pp; English.
XX
CC The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a consensus sequence for a parent protein used to design a savine of the
CC invention
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 78; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAPR 15
||||||||||||||||
Db 48 AGAARASGPGGGAPR 62

Search completed: March 13, 2006, 19:03:59
Job time : 113.941 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:04:24 ; Search time 17.8235 Seconds
(without alignments)
80.975 Million cell updates/sec

Title: US-09-529-206E-26
Perfect score: 78
Sequence: 1 AGAARASGPGGGAPR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR1_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	64.1	82	2	T04476	acclimation protei
2	50	64.1	222	2	T36115	probable oxidoredu
3	49	62.8	351	2	S50754	hypothetical prote
4	48.5	62.2	566	2	T21096	hypothetical prote
5	48.5	62.2	692	2	T21095	hypothetical prote
6	48	61.5	220	2	E72464	hypothetical prote
7	48	61.5	1690	2	T35694	ATP dependent DNA
8	47	60.3	380	2	JC1451	Ca2+/calmodulin-de
9	46	59.0	333	2	C48423	homeotic protein e
10	46	59.0	504	2	AE3526	5-carboxymethyl-2-
11	45	57.7	173	2	AB3648	flagellar basal-bo
12	45	57.7	275	2	C84673	hypothetical prote
13	45	57.7	627	2	A44112	spidroin 2, dragli
14	45	57.7	651	2	A36333	dnaK-type molecula
15	44.5	57.1	335	2	S08341	myristylated alani
16	44.5	57.1	730	2	A36226	collagen alpha 1 c
17	44	56.4	226	1	S51660	histone H1-5 [vali
18	44	56.4	232	1	TVFV10	transforming prote
19	44	56.4	259	2	A44988	transforming prote
20	44	56.4	269	2	A47008	transcription acti
21	44	56.4	286	2	S04673	H+-transporting tw
22	44	56.4	305	1	A49011	c-Crk - chicken
23	44	56.4	309	2	A39169	myristylated alani
24	44	56.4	379	1	A48082	MAP kinase 3 (EC 2
25	44	56.4	510	2	A42750	insulinoma-associa
26	44	56.4	679	2	S02165	regulatory protein
27	44	56.4	900	2	B70694	probable infB - My
28	44	56.4	924	2	F87103	initiation factor
29	44	56.4	954	2	A87431	regulatory protein
30	44	56.4	1134	2	A41350	adenylate cyclase
31	44	56.4	3190	2	T13828	CREB-binding prote
32	43.5	55.8	328	2	A44192	heterogeneous nucl
33	43	55.1	185	2	T36874	hypothetical prote
34	43	55.1	189	2	AE3136	Hypothetical Prote
35	43	55.1	189	2	G98151	hypothetical prote
36	43	55.1	213	2	S42585	DNA-invertase - Rh
37	43	55.1	260	2	T32525	hypothetical prote
38	43	55.1	280	2	D70803	hypothetical prote
39	43	55.1	307	2	B72677	hypothetical prote
40	43	55.1	341	2	JC4051	jun-D protein - ra
41	43	55.1	349	2	S55626	hypothetical prote
42	43	55.1	377	2	S28184	Ca2+/calmodulin-de
43	43	55.1	420	2	A49642	transcription fact
44	43	55.1	431	2	E82766	conserved hypothet
45	43	55.1	437	2	T30220	membrane transport

ALIGNMENTS

RESULT 1
T04476
acclimation protein 2 - barley
C;Species: Hordeum vulgare (barley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04476
R;Phillips, J.R.; Dunn, M.A.; Hughes, M.A.
Plant Mol. Biol. 33, 1013-1023, 1997
A;Title: mRNA stability and localisation of the low temperature responsive barley gene
A;Reference number: Z15367; MUID:97299834; PMID:9154983
A;Accession: T04476
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-82 <PHI>
A;Cross-references: UNIPROT:Q40033; UNIPARC:UPI000009CE5A; EMBL:X97917; NID:g1418969; P
A;Experimental source: cv. Igri
C;Genetics:
A;Gene: blt14.2

Query Match 64.1%; Score 50; DB 2; Length 82;
Best Local Similarity 69.2%; Pred. No. 4.6;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          2 GAARASGPGGGAP 14
              |||| :| ||| |
Db         31 GAARGAGAGGGVP 43
```

RESULT 2
T36115
probable oxidoreductase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C;Accession: T36115
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1999
A;Reference number: Z21597
A;Accession: T36115
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-222 <MUR>
A;Cross-references: UNIPROT:Q9X887; UNIPARC:UPI00000DB008; EMBL:AL049707; PIDN:CAB41281
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCE15.12c
C;Superfamily: NAD(P)H-dependent FMN reductase (sulfate starvation-induced protein 4);

Query Match 64.1%; Score 50; DB 2; Length 222;
Best Local Similarity 64.3%; Pred. No. 11;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 AGAARASGPGGGAP 14
```

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            :|:||||||  | |
Db        180 SGSARASGPSAGRP 193


RESULT 3
S50754
hypothetical protein WP6 - Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S50754
R;Woessner, J.P.; Molendijk, A.J.; van Egmond, P.; Klis, F.M.; Goodenough, U.W.; Haring,
Plant Mol. Biol. 26, 947-960, 1994
A;Title: Domain conservation in several volvocalean cell wall proteins.
A;Reference number: S50754; MUID:95093034; PMID:8000007
A;Accession: S50754
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-351 <WOE>
A;Cross-references: UNIPROT:Q39492; UNIPARC:UPI00000A170A; EMBL:L29028; NID:g530877; PID

  Query Match             62.8%;  Score 49;  DB 2;  Length 351;
  Best Local Similarity   64.3%;  Pred. No. 22;
  Matches    9;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAP 14
              :|: ||| |||| |
Db        295 SGSPRASPPGGGPP 308


RESULT 4
T21096
hypothetical protein F18H3.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21096
R;Coles, L.
submitted to the EMBL Data Library, July 1995
A;Reference number: Z19373
A;Accession: T21096
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-566 <WIL>
A;Cross-references: UNIPROT:Q19581; UNIPARC:UPI0000079311; EMBL:Z50110; PIDN:CAA90446.1;
A;Experimental source: clone F18H3
C;Genetics:
A;Gene: CESP:F18H3.3b
A;Map position: X
A;Introns: 111/1; 215/2; 469/3; 552/3
C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology

  Query Match             62.2%;  Score 48.5;  DB 2;  Length 566;
  Best Local Similarity   64.7%;  Pred. No. 38;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 AGAARASGPG---GGAP 14
              ||| |  |||   ||||
Db        533 AGAPRVGGPGVQMGGAP 549


RESULT 5
T21095
hypothetical protein F18H3.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21095
R;Coles, L.
submitted to the EMBL Data Library, July 1995
A;Reference number: Z19373
A;Accession: T21095
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-692 <WIL>
A;Cross-references: UNIPROT:Q19579; UNIPARC:UPI0000079A30; EMBL:Z50110; PIDN:CAA90444.1;
A;Experimental source: clone F18H3
C;Genetics:
A;Gene: CESP:F18H3.3a
A;Map position: X
A;Introns: 111/1; 215/2; 469/3; 552/3
C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology

  Query Match             62.2%;  Score 48.5;  DB 2;  Length 692;
  Best Local Similarity   64.7%;  Pred. No. 45;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 AGAARASGPG---GGAP 14
              ||| |  |||   ||||
Db        533 AGAPRVGGPGVQMGGAP 549


RESULT 6
E72464
hypothetical protein APE2360 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: E72464
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: E72464
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-220 <KAW>
A;Cross-references: UNIPROT:Q9Y9C7; UNIPARC:UPI000005E2F9; DDBJ:AP000064; NID:g5105945;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE2360
C;Superfamily: Aeropyrum pernix hypothetical protein APE2360

  Query Match             61.5%;  Score 48;  DB 2;  Length 220;
  Best Local Similarity   60.0%;  Pred. No. 20;
  Matches    9;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              ||| | : ||||: |
Db        181 AGATRVARPGGGSDR 195


RESULT 7
T35694
ATP dependent DNA helicase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35694
R;Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A;Reference number: Z21587
A;Accession: T35694
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1690 <HAR>
A;Cross-references: UNIPROT:O86821; UNIPARC:UPI00000DACB6; EMBL:AL031031; PIDN:CAA19862
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC7C7.16c

  Query Match             61.5%;  Score 48;  DB 2;  Length 1690;
  Best Local Similarity   64.3%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 GAARASGPGGGAPR 15
              |:|  ||| | |||
Db       1437 GSANGSGPEGSAPR 1450
```

```
RESULT 8
JC1451
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) - rat
N;Alternate names: ERK1-MAP kinase; extracellular signal-regulated kinase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JC1451; A35061; A37140; A40466; S24947
R;Marquardt, B.; Stabel, S.
Gene 120, 297-299, 1992
A;Title: Sequence of a rat cDNA encoding the ERK1-MAP kinase.
A;Reference number: JC1451; MUID:93013050; PMID:1327976
A;Accession: JC1451
A;Molecule type: mRNA
A;Residues: 1-380 <MAR>
A;Cross-references: UNIPROT:P21708; UNIPARC:UPI000012F174; EMBL:X65198; NID:g56626; PIDN
A;Experimental source: brain
R;Boulton, T.G.; Yancopoulos, G.D.; Gregory, J.S.; Slaughter, C.; Moomaw, C.; Hsu, J.; C
Science 249, 64-67, 1990
A;Title: An insulin-stimulated protein kinase similar to yeast kinases involved in cell
A;Reference number: A35061; MUID:90312137; PMID:2164259
A;Accession: A35061
A;Molecule type: mRNA
A;Residues: 14-380 <BOU>
A;Cross-references: UNIPARC:UPI0000145072; GB:M38194; NID:g204051; PIDN:AAA41123.1; PID:
R;Boulton, T.G.; Gregory, J.S.; Cobb, M.H.
Biochemistry 30, 278-286, 1991
A;Title: Purification and properties of extracellular signal-regulated kinase 1, an insu
A;Reference number: A37140; MUID:91105092; PMID:1846291
A;Accession: A37140
A;Status: preliminary
A;Molecule type: protein
A;Residues: 43-64;167-178,'X',180-183,'X',185 <BO2>
A;Cross-references: UNIPARC:UPI000017558F; UNIPARC:UPI0000175590
R;De Miguel, C.; Kligman, D.; Patel, J.; Detera-Wadleigh, S.D.
DNA Cell Biol. 10, 505-514, 1991
A;Title: Molecular analysis of microtubule-associated protein-2 kinase cDNA from mouse a
A;Reference number: A40466; MUID:91369479; PMID:1716439
A;Accession: A40466
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 14-94,'R',96-380 <DEM>
A;Cross-references: UNIPARC:UPI00001707CE; GB:U12008; GB:S59509; NID:g515498; PIDN:AAA20
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; calmodulin binding; phosphoprotein; phosphotransferase; serine/threonin
F;41-331/Domain: protein kinase homology <KIN>
F;49-57/Region: protein kinase ATP-binding motif

  Query Match             60.3%;  Score 47;  DB 2;  Length 380;
  Best Local Similarity   66.7%;  Pred. No. 42;
  Matches   10;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              | || | | ||| ||
Db          2 AAAAAAPGGGGGEPR 16


RESULT 9
C48423
homeotic protein engrailed 1 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
C;Accession: C48423
R;Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.; Joyner, A.I
Dev. Genet. 13, 345-358, 1992
A;Title: Cloning and sequence comparison of the mouse, human, and chicken engrailed gene
A;Reference number: A48423; MUID:93185339; PMID:1363401
A;Accession: C48423
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-333 <LOG>
A;Cross-references: UNIPARC:UPI000017A297
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;245-301/Domain: homeobox homology <HOX>

  Query Match             59.0%;  Score 46;  DB 2;  Length 333;
  Best Local Similarity   64.3%;  Pred. No. 51;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAP 14
              ||||:| | ||  |
Db        166 AGAAKAQGDGGETP 179


RESULT 10
AE3526
5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase (EC 1.2.1.-) [imported] -
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AE3526
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten
A;Reference number: AD3252; PMID:11756688
A;Accession: AE3526
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-504 <KUR>
A;Cross-references: UNIPROT:Q8YDP0; UNIPARC:UPI0000058376; GB:AE008918; PIDN:AAL53376.1
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII0135
A;Map position: II
C;Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
C;Keywords: oxidoreductase

  Query Match             59.0%;  Score 46;  DB 2;  Length 504;
  Best Local Similarity   66.7%;  Pred. No. 73;
  Matches    8;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGG 12
              || |: :|||||
Db        366 AGGAKFAGPGGG 377


RESULT 11
AB3648
flagellar basal-body rod protein flgF [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AB3648
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten
A;Reference number: AD3252; PMID:11756688
A;Accession: AB3648
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <KUR>
A;Cross-references: UNIPROT:Q8YAZ4; UNIPARC:UPI0000058740; GB:AE008918; PIDN:AAL54349.1
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII1107
A;Map position: II

  Query Match             57.7%;  Score 45;  DB 2;  Length 173;
  Best Local Similarity   64.3%;  Pred. No. 39;
  Matches    9;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 GAARASGPGGGAPR 15
              ||     |||||||
Db        125 GAPIVLNPGGGAPR 138


RESULT 12
```

C84673
hypothetical protein At2g27470 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: C84673
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84673
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-275 <STO>
A;Cross-references: UNIPROT:Q9ZQH2; UNIPARC:UPI000000C26F; GB:AE002093; NID:g4314389; PI
C;Genetics:
A;Gene: At2g27470
A;Map position: 2

Query Match 57.7%; Score 45; DB 2; Length 275;
Best Local Similarity 76.9%; Pred. No. 59;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGA 13
|||| || | |||
Db 107 AGAAAASYPAGGA 119

RESULT 13
A44112
spidroin 2, dragline silk fibroin - orb spider (Nephila clavipes) (fragment)
N;Alternate names: silk fibroin, dragline
C;Species: Nephila clavipes
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A44112; S27824
R;Hinman, M.B.; Lewis, R.V.
J. Biol. Chem. 267, 19320-19324, 1992
A;Title: Isolation of a clone encoding a second dragline silk fibroin. Nephila clavipes
A;Reference number: A44112; MUID:92406876; PMID:1527052
A;Accession: A44112
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-627 <HIN>
A;Cross-references: UNIPROT:P46804; UNIPARC:UPI0000135DC6; GB:M92913; NID:g159713; PID:g
A;Note: sequence extracted from NCBI backbone (NCBIP:113893)
R;Hinman, M.B.; Lewis, R.V.
submitted to the EMBL Data Library, May 1992
A;Description: Isolation of a clone encoding a second dragline silk fibroin: Nephila cla
A;Reference number: S27824
A;Accession: S27824
A;Molecule type: mRNA
A;Residues: 19-627 <HI2>
A;Cross-references: UNIPARC:UPI000017BE0B; EMBL:M92913

Query Match 57.7%; Score 45; DB 2; Length 627;
Best Local Similarity 64.3%; Pred. No. 1.2e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAP 14
| || |:|||| |
Db 30 AAAAAAAGPGGYGP 43

RESULT 14
A36333
dnaK-type molecular chaperone Hsc70-4 - fruit fly (Drosophila melanogaster)
N;Alternate names: heat shock cognate protein 70
C;Species: Drosophila melanogaster
C;Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 31-Dec-2004
C;Accession: A36333
R;Perkins, L.A.; Doctor, J.S.; Zhang, K.; Stinson, L.; Perrimon, N.; Craig, E.A.
Mol. Cell. Biol. 10, 3232-3238, 1990
A;Title: Molecular and developmental characterization of the heat shock cognate 4 gene c
A;Reference number: A36333; MUID:90258915; PMID:2111451
A;Accession: A36333
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-651 <PER>
A;Cross-references: UNIPROT:P11147; UNIPARC:UPI000016BC3E; GB:M36114; NID:g157663; PIDN
C;Genetics:
A;Gene: FlyBase:Hsc70-4
A;Cross-references: FlyBase:FBgn0001219
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: bcr protein
C;Keywords: ATP; molecular chaperone; nucleus

Query Match 57.7%; Score 45; DB 2; Length 651;
Best Local Similarity 64.3%; Pred. No. 1.2e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAP 14
|||| |:| || |
Db 632 AGAAGAAGAGGAGP 645

RESULT 15
S08341
myristylated alanine-rich protein kinase C substrate - bovine
N;Alternate names: acidic calmodulin-binding 81K protein (ACAMP-81); MARCKS
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S08341; A32904; S29270; A46098; PS0338
R;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
Nucleic Acids Res. 17, 3987-3988, 1989
A;Title: Nucleotide sequence of a cDNA for the bovine myristoylated alanine-rich C kinas
A;Reference number: S08341; MUID:89282412; PMID:2734111
A;Accession: S08341
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-335 <STU>
A;Cross-references: UNIPROT:P12624; UNIPARC:UPI000016C340; EMBL:M24638; NID:g163339; PID
R;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 4012-4016, 1989
A;Title: Molecular cloning, characterization, and expression of a cDNA encoding the "80-
A;Reference number: A32904; MUID:89264553; PMID:2726763
A;Accession: A32904
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-98,'Q',100-335 <ST2>
A;Cross-references: UNIPARC:UPI000017750A; GB:M24638; GB:M23738
R;Herget, T.; Brooks, S.F.; Broad, S.; Rozengurt, E.
Eur. J. Biochem. 209, 7-14, 1992
A;Title: Relationship between the major protein kinase C substrates acidic 80-kDa protei
or equivalent genes in different species.
A;Reference number: S29267; MUID:93011168; PMID:1396720
A;Accession: S29270
A;Molecule type: DNA
A;Residues: 191-253,'SEE',257-279,283-292,'V',294,'PEQE',299,'A',300,'A',302-313,'A',315
A;Cross-references: UNIPARC:UPI000017750B
R;Manenti, S.; Sorokine, O.; Van Dorsselaer, A.; Taniguchi, H.
J. Biol. Chem. 268, 6878-6881, 1993
A;Title: Isolation of the non-myristoylated form of a major substrate of protein kinase
A;Reference number: A46098; MUID:93216617; PMID:8463217
A;Accession: A46098
A;Molecule type: protein
A;Residues: 2-11 <MAN>
A;Cross-references: UNIPARC:UPI000017750C
R;Mizutani, A.; Tokumitsu, H.; Hidaka, H.
Biochem. Biophys. Res. Commun. 182, 1395-1401, 1992
A;Title: Acidic calmodulin binding protein, ACAMP-81, is MARCKS protein interacting with
A;Reference number: PS0338; MUID:92171958; PMID:1540183
A;Accession: PS0338
A;Molecule type: protein
A;Residues: 12-30;56-69;88-98,'AS',100-103;104-109,'E',111-123;156-160;165-171;196-215;2

A;Cross-references: UNIPARC:UPI000017750D; UNIPARC:UPI000017750E; UNIPARC:UPI000017750F;
514
A;Experimental source: brain
A;Note: this sequence is identical with that of myristoylated alanine-rich C-kinase subs
C;Comment: This protein is a major cellular substrate for protein kinase C and plays a r
C;Comment: It binds to calmodulin in one to one molar ratio in the presence of calcium a
C;Genetics:
A;Introns: 34/3
C;Superfamily: neurofilament triplet H protein
C;Keywords: actin binding; blocked amino end; calmodulin binding; lipoprotein; myristyla
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;158,162,166,169/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status

  Query Match 57.1%; Score 44.5; DB 2; Length 335;
  Best Local Similarity 54.2%; Pred. No. 81;
  Matches 13; Conservative 1; Mismatches 1; Indels 9; Gaps 2;

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Qy          1 AGAA-----RASGPG----GGAPR 15
              ||||      |:|||    |||||
Db        278 AGAAGCEAPSAAGPGCPRAGGAPR 301
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Search completed: March 13, 2006, 19:16:10
Job time : 19.8235 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 18:53:23 ; Search time 108.882 Seconds
(without alignments)
97.196 Million cell updates/sec

Title: US-09-529-206E-26
Perfect score: 78
Sequence: 1 AGAARASGPGGGAPR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	78	100.0	142	2	Q9NY13_HUMAN	Q9ny13 homo sapien
2	78	100.0	180	1	CTG1B_HUMAN	P78358 homo sapien
3	78	100.0	180	2	Q7LBY4_HUMAN	Q7lby4 homo sapien
4	70	89.7	210	1	CTAG2_HUMAN	O75638 homo sapien
5	55	70.5	337	1	CT086_HUMAN	Q9bz19 homo sapien
6	55	70.5	559	2	Q8L680_ORYSA	Q8l680 oryza sativ
7	55	70.5	867	2	Q94LD1_ORYSA	Q94ld1 oryza sativ
8	54	69.2	362	2	Q63QT8_BURPS	Q63qt8 burkholderi
9	54	69.2	362	2	Q62H22_BURMA	Q62h22 burkholderi
10	54	69.2	895	2	Q4NUK4_9DELT	Q4nuk4 anaeromyxob
11	53	67.9	321	2	Q96S27_HUMAN	Q96s27 homo sapien
12	53	67.9	322	2	Q67PJ0_SYMTH	Q67pj0 symbiobacte
13	53	67.9	644	2	Q688J5_ORYSA	Q688j5 oryza sativ
14	53	67.9	1379	2	Q7QEK5_ANOGA	Q7qek5 anopheles g
15	52.5	67.3	924	2	Q4NQS2_9DELT	Q4nqs2 anaeromyxob
16	52	66.7	447	2	Q9GRA8_GRYBI	Q9gra8 gryllus bim
17	52	66.7	786	2	Q4QCF3_LEIMA	Q4qcf3 leishmania
18	52	66.7	3288	2	Q7T5D9_CHV1	Q7t5d9 cercopithec
19	52	66.7	3326	2	Q7T591_CHV1	Q7t591 cercopithec
20	51	65.4	367	2	Q6AV33_ORYSA	Q6av33 oryza sativ
21	51	65.4	405	2	Q4JWB8_CORJK	Q4jwb8 corynebacte
22	51	65.4	472	2	Q5C8R1_9ADEN	Q5c8r1 simian aden
23	51	65.4	880	2	Q63K38_BURPS	Q63k38 burkholderi
24	51	65.4	926	1	CEZ2_MOUSE	Q8r554 mus musculu
25	51	65.4	1031	2	Q75IL4_ORYSA	Q75il4 oryza sativ
26	50.5	64.7	108	2	Q8H321_ORYSA	Q8h321 oryza sativ
27	50	64.1	82	2	Q40033_HORVU	Q40033 hordeum vul
28	50	64.1	102	2	Q4R9N8_TETNG	Q4r9n8 tetraodon n
29	50	64.1	111	2	Q5NTA5_CANFA	Q5nta5 canis famil
30	50	64.1	194	2	Q96BU2_HUMAN	Q96bu2 homo sapien
31	50	64.1	222	2	Q9X887_STRCO	Q9x887 streptomyce
32	50	64.1	341	2	Q6H6A6_ORYSA	Q6h6a6 oryza sativ
33	50	64.1	550	2	Q86PI1_TOXGO	Q86pi1 toxoplasma
34	50	64.1	896	2	Q96D18_HUMAN	Q96d18 homo sapien
35	50	64.1	1253	2	Q6DHV6_HUMAN	Q6dhv6 homo sapien
36	50	64.1	1430	2	Q9H7P9_HUMAN	Q9h7p9 homo sapien
37	50	64.1	1787	2	Q9M4X9_CHLRE	Q9m4x9 chlamydomon
38	49.5	63.5	835	1	NLGN2_HUMAN	Q8nfz4 homo sapien
39	49.5	63.5	836	1	NLGN2_RAT	Q62888 rattus norv
40	49.5	63.5	836	2	Q5F288_MOUSE	Q5f288 mus musculu
41	49.5	63.5	884	2	Q69ZK9_MOUSE	Q69zk9 mus musculu
42	49	62.8	160	2	Q94LU4_ORYSA	Q94lu4 oryza sativ
43	49	62.8	172	2	Q9DCH0_MOUSE	Q9dch0 mus musculu
44	49	62.8	175	1	PACA_CHICK	P41534 g glucagon-
45	49	62.8	327	2	Q63HT9_BURPS	Q63ht9 burkholderi

ALIGNMENTS

RESULT 1
Q9NY13_HUMAN
ID Q9NY13_HUMAN PRELIMINARY; PRT; 142 AA.
AC Q9NY13;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein LAGE-2 (Fragment).
GN Name=LAGE-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ275978; CAB76945.1; -; mRNA.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;

Query Match 100.0%; Score 78; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         22 AGAARASGPGGGAPR 36
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RESULT 2
CTG1B_HUMAN
ID CTG1B_HUMAN STANDARD; PRT; 180 AA.
AC P78358;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-
DE ESO-1).
GN Name=CTAG1B; Synonyms=CTAG, CTAG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
RA Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,
RA Williamson B., Stockert E., Pfreundschuh M., Old L.J.;
RT "A testicular antigen aberrantly expressed in human cancers detected
RT by autologous antibody screening.";

```
RL   Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Melanoma;
RX   MEDLINE=98289662; PubMed=9626360;
RA   Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA   de Plaen E., Boon T.;
RT   "LAGE-1, a new gene with tumor specificity.";
RL   Int. J. Cancer 76:903-908(1998).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98430682; PubMed=9759882;
RA   Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,
RA   Schwartzentruber D.J., Rosenberg S.A.;
RT   "A breast and melanoma-shared tumor antigen: T cell responses to
RT   antigenic peptides translated from different open reading frames.";
RL   J. Immunol. 161:3596-3606(1998).
CC   -!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide
CC       variety of cancers. Detected in uterine myometrium.
CC   -!- SIMILARITY: Belongs to the CTAG family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U87459; AAB49693.1; -; mRNA.
DR   EMBL; AJ003149; CAA05908.1; -; mRNA.
DR   EMBL; AF038567; AAD05202.1; -; mRNA.
DR   HGNC; HGNC:2491; CTAG1B.
DR   MIM; 300156; -.
KW   Antigen; Transmembrane.
FT   TRANSMEM    156    172       Potential.
FT   COMPBIAS      5     82       Gly-rich.
SQ   SEQUENCE   180 AA;  17992 MW;  B122C5C2C8BE1569 CRC64;

  Query Match             100.0%;  Score 78;  DB 1;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.015;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 3
Q7LBY4_HUMAN
ID   Q7LBY4_HUMAN PRELIMINARY;      PRT;   180 AA.
AC   Q7LBY4;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
DE   antigen 1-A).
GN   Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21303268;
RA   Galgoczy P., Rosenthal A., Platzer M.;
RT   "Human-mouse comparative sequence analysis of the NEMO gene reveals an
RT   alternative promoter within the neighboring G6PD gene.";
RL   Gene 271:93-98(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21566154; PubMed=11709543; DOI=10.1093/hmg/10.22.2557;
RA   Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
RA   Patlan H., Ciccodicola A., Kenwrick S., Platzer M., D'Urso M.,
RA   Nelson D.L.;
RT   "Multiple pathogenic and benign genomic rearrangements occur at a 35
RT   kb duplication involving the NEMO and LAGE2 genes.";
RL   Hum. Mol. Genet. 10:2557-2567(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Platzer M.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Platzer M.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RA   Galgoczy P., Platzer M.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99454989; PubMed=10523621;
RA   De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
RT   "DNA methylation is the primary silencing mechanism for a set of germ
RT   line- and tumor-specific genes with a CpG-rich promoter.";
RL   Mol. Cell. Biol. 19:7327-7335(1999).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RA   Lethe B.G.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF277315; AAL27014.1; -; Genomic_DNA.
DR   EMBL; AJ275977; CAB76943.1; -; Genomic_DNA.
DR   EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
SQ   SEQUENCE   180 AA;  17992 MW;  B122C5C2C8BE1569 CRC64;

  Query Match             100.0%;  Score 78;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.015;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 4
CTAG2_HUMAN
ID   CTAG2_HUMAN    STANDARD;      PRT;   210 AA.
AC   O75638; O75637; Q9BU80; Q9UJ89; Q9Y479;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
GN   Name=CTAG2; Synonyms=ESO2, LAGE1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B).
RC   TISSUE=Melanoma;
RX   MEDLINE=98289662; PubMed=9626360;
RA   Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA   de Plaen E., Boon T.;
RT   "LAGE-1, a new gene with tumor specificity.";
RL   Int. J. Cancer 76:903-908(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B), AND VARIANTS
RP   GLN-6; GLN-89 AND ARG-138.
RC   TISSUE=Melanoma;
RX   MEDLINE=99325550; PubMed=10399963;
RA   Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT   "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT   unexpected translation product of LAGE-1.";
RL   Int. J. Cancer 82:442-448(1999).
RN   [3]
```

```
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
RP   ARG-138.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=LAGE-1B; Synonyms=LAGE-1L;
CC         IsoId=O75638-1; Sequence=Displayed;
CC       Name=LAGE-1A; Synonyms=LAGE-1S;
CC         IsoId=O75638-2; Sequence=VSP_004301;
CC   -!- TISSUE SPECIFICITY: Testis and very low level in placenta and in
CC       some uterus samples. Observed in 25-50% of tumor samples of
CC       melanomas, non-small-cell lung carcinomas, bladder, prostate and
CC       head and neck cancers.
CC   -!- DOMAIN: A transmembrane domain is present in isoform LAGE-1A.
CC   -!- SIMILARITY: Belongs to the CTAG family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AJ223093; CAA11117.1; -; Genomic_DNA.
DR   EMBL; AJ223093; CAA11116.1; -; Genomic_DNA.
DR   EMBL; AJ223040; CAA11043.1; -; mRNA.
DR   EMBL; AJ223041; CAA11044.1; -; mRNA.
DR   EMBL; AJ012834; CAA10194.1; -; mRNA.
DR   EMBL; AJ012835; CAA10196.1; -; mRNA.
DR   EMBL; BC002833; AAH02833.1; -; mRNA.
DR   Ensembl; ENSG00000126890; Homo sapiens.
DR   HGNC; HGNC:2492; CTAG2.
DR   H-InvDB; HIX0017163; -.
DR   MIM; 300396; -.
KW   Alternative splicing; Antigen; Polymorphism; Transmembrane.
FT   COMPBIAS      5     79       Gly-rich.
FT   COMPBIAS    183    188       Poly-Pro.
FT   VARSPLIC    135    210       MSVWDQDREGAGRMRVVGWGLGSASPEGQKARDLRTPKHKV
FT                                SEQRPGTPGPPPPEGAQGDGCRGVAFNVMFSAPHI -> IR
FT                                LTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQAPSG
FT                                QRR (in isoform LAGE-1A).
FT                                /FTId=VSP_004301.
FT   VARIANT       6      6       R -> Q.
FT                                /FTId=VAR_007855.
FT   VARIANT      89     89       E -> Q.
FT                                /FTId=VAR_007856.
FT   VARIANT     138    138       W -> R.
FT                                /FTId=VAR_007857.
SQ   SEQUENCE   210 AA;  21120 MW;  8BE0EE00AE55E8BE CRC64;

  Query Match             89.7%;  Score 70;  DB 1;  Length 210;
  Best Local Similarity   93.3%;  Pred. No. 0.19;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              ||||||||| |||||
Db         48 AGAARASGPRGGAPR 62


RESULT 5
CT086_HUMAN
ID   CT086_HUMAN     STANDARD;      PRT;   337 AA.
AC   Q9BZ19;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Hypothetical protein C20orf86.
GN   Name=C20orf86;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA   Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA   Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA   Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA   Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA   Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA   Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA   Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA   Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA   Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA   Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA   Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA   Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
CC   -!- SIMILARITY: Contains 2 ANK repeats.
CC   -!- SIMILARITY: Contains 1 ubiquitin-like domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AL354776; CAC17565.2; -; Genomic_DNA.
DR   HSSP; P42771; 2A5E.
DR   Ensembl; ENSG00000124227; Homo sapiens.
DR   HGNC; HGNC:16217; C20orf86.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR000626; Ubiquitin.
DR   Pfam; PF00023; Ank; 2.
DR   PRINTS; PR01415; ANKYRIN.
DR   SMART; SM00248; ANK; 2.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 2.
DR   PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
DR   PROSITE; PS50053; UBIQUITIN_2; 1.
KW   ANK repeat; Hypothetical protein; Polymorphism; Repeat.
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FT   DOMAIN       88    164       Ubiquitin-like.
FT   REPEAT      211    241       ANK 1.
FT   REPEAT      244    273       ANK 2.
FT   VARIANT     287    287       R -> C (in dbSNP:584855).
FT                                /FTId=VAR_014400.
SQ   SEQUENCE   337 AA;  36714 MW;  EC8BA4AD414756CB CRC64;

  Query Match             70.5%;  Score 55;  DB 1;  Length 337;
  Best Local Similarity   73.3%;  Pred. No. 27;
  Matches   11;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              || |||:|| ||| |
Db          8 AGGARAAGPTGGASR 22


RESULT 6
Q8L680_ORYSA
ID   Q8L680_ORYSA PRELIMINARY;      PRT;   559 AA.
AC   Q8L680;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Hypothetical protein OSJNBa0011L09.12.
GN   ORFNames=OSJNBa0011L09.12;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA   Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
RA   Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
RA   Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA   Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell R.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   The Rice Chromosome 10 Sequencing Consortium;
RT   "In-depth view of structure, activity, and evolution of rice
RT   chromosome 10.";
RL   Science 300:1566-1569(2003).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC092388; AAM22719.1; -; Genomic_DNA.
DR   EMBL; AE017090; AAP53592.1; -; Genomic_DNA.
DR   Gramene; Q8L680; -.
DR   InterPro; IPR007228; DUF390.
DR   InterPro; IPR007321; Transposase_28.
DR   Pfam; PF04094; DUF390; 2.
DR   Pfam; PF04195; Transposase_28; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   559 AA;  58950 MW;  A5B4492C2D3F94FA CRC64;

  Query Match             70.5%;  Score 55;  DB 2;  Length 559;
  Best Local Similarity   66.7%;  Pred. No. 42;
  Matches   10;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              || :| ||||||  |
Db        276 AGGSRTSGPGGGGSR 290


RESULT 7
Q94LD1_ORYSA
ID   Q94LD1_ORYSA PRELIMINARY;      PRT;   867 AA.
AC   Q94LD1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein OSJNBa0026A15.11.
GN   Name=OSJNBa0026A15.11;
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
RA   Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
RA   Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.E.,
RA   Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
RA   White O., Fraser C.M.;
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC084404; AAK50601.1; -; Genomic_DNA.
DR   Gramene; Q94LD1; -.
DR   InterPro; IPR007228; DUF390.
DR   InterPro; IPR007321; Transposase_28.
DR   Pfam; PF04094; DUF390; 3.
DR   Pfam; PF04195; Transposase_28; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   867 AA;  92812 MW;  7365009715EDDC21 CRC64;

  Query Match             70.5%;  Score 55;  DB 2;  Length 867;
  Best Local Similarity   66.7%;  Pred. No. 63;
  Matches   10;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              || :|| |||||  |
Db        205 AGGSRAGGPGGGGSR 219


RESULT 8
Q63QT8_BURPS
ID   Q63QT8_BURPS PRELIMINARY;      PRT;   362 AA.
AC   Q63QT8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative DNA polymerase III.
GN   OrderedLocusNames=BPSL2936;
OS   Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia; pseudomallei group.
OX   NCBI_TaxID=28450;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=K96243;
RX   PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA   Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
RA   Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA   Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
RA   Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA   Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D.,
RA   Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA   Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA   Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA   Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA   Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT   "Genomic plasticity of the causative agent of melioidosis,
RT   Burkholderia pseudomallei.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR   EMBL; BX571965; CAH36946.1; -; Genomic_DNA.
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DR   GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR   GO; GO:0006260; P:DNA replication; IEA.
DR   InterPro; IPR010372; DNA_pol3_delta.
DR   InterPro; IPR005790; DNA_polIII_delta.
DR   Pfam; PF06144; DNA_pol3_delta; 1.
DR   TIGRFAMs; TIGR01128; holA; 1.
KW   Complete proteome.
SQ   SEQUENCE   362 AA;  38726 MW;  D5FF3DE783D41E41 CRC64;

  Query Match             69.2%;  Score 54;  DB 2;  Length 362;
  Best Local Similarity   83.3%;  Pred. No. 38;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ARASGPGGGAPR 15
              |||:|||| |||
Db        348 ARAAGPGGDAPR 359


RESULT 9
Q62H22_BURMA
ID   Q62H22_BURMA PRELIMINARY;      PRT;   362 AA.
AC   Q62H22;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   DNA polymerase III, delta subunit (EC 2.7.7.7).
GN   Name=holA; OrderedLocusNames=BMA2451;
OS   Burkholderia mallei (Pseudomonas mallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia.
OX   NCBI_TaxID=13373;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ATCC 23344;
RX   PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA   Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA   Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA   Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA   Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA   Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
RA   Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA   Zafar N., Zhou L., Fraser C.M.;
RT   "Structural flexibility in the Burkholderia mallei genome.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR   EMBL; CP000010; AAU49707.1; -; Genomic_DNA.
DR   TIGR; BMA2451; -.
DR   GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006260; P:DNA replication; IEA.
DR   InterPro; IPR010372; DNA_pol3_delta.
DR   InterPro; IPR005790; DNA_polIII_delta.
DR   Pfam; PF06144; DNA_pol3_delta; 1.
DR   TIGRFAMs; TIGR01128; holA; 1.
KW   Complete proteome; Nucleotidyltransferase; Transferase.
SQ   SEQUENCE   362 AA;  38726 MW;  D5FF3DE783D41E41 CRC64;

  Query Match             69.2%;  Score 54;  DB 2;  Length 362;
  Best Local Similarity   83.3%;  Pred. No. 38;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 ARASGPGGGAPR 15
              |||:|||| |||
Db        348 ARAAGPGGDAPR 359


RESULT 10
Q4NUK4_9DELT
ID   Q4NUK4_9DELT PRELIMINARY;      PRT;   895 AA.
AC   Q4NUK4;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   LigA.
GN   ORFNames=AdehDRAFT_2813;
OS   Anaeromyxobacter dehalogenans 2CP-C.
OC   Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC   Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
OX   NCBI_TaxID=290397;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=2CP-C;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome assembly of Anaeromyxobacter
RT   dehalogenans 2CP-C.";
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=2CP-C;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Anaeromyxobacter
RT   dehalogenans 2CP-C.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAHD01000013; EAL79351.1; -; Genomic_DNA.
SQ   SEQUENCE   895 AA;  93871 MW;  0AE25BBBF172BDB0 CRC64;

  Query Match             69.2%;  Score 54;  DB 2;  Length 895;
  Best Local Similarity   73.3%;  Pred. No. 88;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              | | || | ||||||
Db        795 AAARRARGAGGGAPR 809


RESULT 11
Q96S27_HUMAN
ID   Q96S27_HUMAN PRELIMINARY;      PRT;   321 AA.
AC   Q96S27;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein gene X.
GN   Name=gene X;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21096910; PubMed=11157797; DOI=10.1093/hmg/10.4.339;
RA   Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA   Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA   Higgs D.R.;
RT   "Sequence, structure and pathology of the fully annotated terminal 2
RT   Mb of the short arm of human chromosome 16.";
RL   Hum. Mol. Genet. 10:339-352(2001).
DR   EMBL; AE006463; AAK61225.1; -; Genomic_DNA.
DR   Ensembl; ENSG00000167933; Homo sapiens.
KW   Hypothetical protein.
SQ   SEQUENCE   321 AA;  32979 MW;  9C8764CFA17F4CD4 CRC64;

  Query Match             67.9%;  Score 53;  DB 2;  Length 321;
  Best Local Similarity   66.7%;  Pred. No. 47;
  Matches   10;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              : ||| :|||||| |
Db          3 SAAARRAGPGGGAAR 17
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RESULT 12
Q67PJ0_SYMTH
ID   Q67PJ0_SYMTH PRELIMINARY;      PRT;   322 AA.
AC   Q67PJ0;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Prephenate dehydrogenase.
GN   OrderedLocusNames=STH1418;
OS   Symbiobacterium thermophilum.
OC   Bacteria; Actinobacteria; Symbiobacterium.
OX   NCBI_TaxID=2734;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=IAM14863;
RX   PubMed=15383646; DOI=10.1093/nar/gkh830;
RA   Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
RA   Morimura K., Ikeda H., Hattori M., Beppu T.;
RT   "Genome sequence of Symbiobacterium thermophilum, an uncultivable
RT   bacterium that depends on microbial commensalism.";
RL   Nucleic Acids Res. 32:4937-4944(2004).
DR   EMBL; AP006840; BAD40403.1; -; Genomic_DNA.
DR   GO; GO:0004665; F:prephenate dehydrogenase (NADP+) activity; IEA.
DR   GO; GO:0006571; P:tyrosine biosynthesis; IEA.
DR   InterPro; IPR003099; Prephen_dehydrog.
DR   Pfam; PF02153; PDH; 1.
KW   Complete proteome.
SQ   SEQUENCE   322 AA;  32843 MW;  09A06AC0AFA734EC CRC64;

  Query Match             67.9%;  Score 53;  DB 2;  Length 322;
  Best Local Similarity   84.6%;  Pred. No. 47;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGA 13
              | || ||||||||
Db         43 AAAADASGPGGGA 55


RESULT 13
Q688J5_ORYSA
ID   Q688J5_ORYSA PRELIMINARY;      PRT;   644 AA.
AC   Q688J5;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein OSJNBb0012G21.2.
GN   Name=OSJNBb0012G21.2;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA   Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA   Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA   Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA   Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA   Wu H.-P., Shaw J.-F.;
RT   "Oryza sativa BAC OSJNBb0012G21 genomic sequence.";
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC135421; AAU10755.1; -; Genomic_DNA.
DR   Gramene; Q688J5; -.
DR   GO; GO:0004057; F:arginyltransferase activity; IEA.
DR   GO; GO:0016598; P:protein arginylation; IEA.
DR   GO; GO:0042176; P:regulation of protein catabolism; IEA.
DR   InterPro; IPR007472; ATE_C.
DR   InterPro; IPR007471; ATE_N.
DR   Pfam; PF04377; ATE_C; 1.
DR   Pfam; PF04376; ATE_N; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   644 AA;  72444 MW;  DDB97FC0C40C23F8 CRC64;

  Query Match             67.9%;  Score 53;  DB 2;  Length 644;
  Best Local Similarity   83.3%;  Pred. No. 88;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGG 12
              :||| |||||||
Db          8 SGAASASGPGGG 19


RESULT 14
Q7QEK5_ANOGA
ID   Q7QEK5_ANOGA PRELIMINARY;      PRT;  1379 AA.
AC   Q7QEK5;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ENSANGP00000004747 (Fragment).
GN   ORFNames=ENSANGG00000003703;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC   Anophelinae; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RT   "Anopheles gambiae re-annotation.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008846; EAA06518.2; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0008305; C:integrin complex; IEA.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR   GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR   InterPro; IPR000413; Integrin_alpha.
DR   Pfam; PF01839; FG-GAP; 3.
DR   Pfam; PF00357; Integrin_alpha; 1.
DR   PRINTS; PR01185; INTEGRINA.
DR   SMART; SM00191; Int_alpha; 6.
KW   Cell adhesion; Integrin; Transmembrane.
FT   NON_TER       1      1
SQ   SEQUENCE   1379 AA;  149836 MW;  2D6945E834F3DD75 CRC64;

  Query Match             67.9%;  Score 53;  DB 2;  Length 1379;
  Best Local Similarity   71.4%;  Pred. No. 1.7e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAP 14
              ||  | |||||| |
Db       1168 AGQLRRSGPGGGPP 1181


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ID   Q4NQS2_9DELT PRELIMINARY;      PRT;   924 AA.
AC   Q4NQS2;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
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DE   Hypothetical protein.
GN   ORFNames=AdehDRAFT_1169;
OS   Anaeromyxobacter dehalogenans 2CP-C.
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OC   Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC   Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
OX   NCBI_TaxID=290397;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=2CP-C;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome assembly of Anaeromyxobacter
RT   dehalogenans 2CP-C.";
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=2CP-C;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Anaeromyxobacter
RT   dehalogenans 2CP-C.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAHD01000032; EAL77965.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   924 AA;  98272 MW;  BE64DCCA32A46FA4 CRC64;

  Query Match             67.3%;  Score 52.5;  DB 2;  Length 924;
  Best Local Similarity   59.1%;  Pred. No. 1.4e+02;
  Matches   13;  Conservative    1;  Mismatches    1;  Indels    7;  Gaps    1;

Qy          1 AGAARASGPG-------GGAPR 15
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Db        713 AGAARAAGGGAAPGVDRGGAPR 734


Search completed: March 13, 2006, 19:14:26
Job time : 111.882 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:14:49 ; Search time 27.8824 Seconds
(without alignments)
44.477 Million cell updates/sec

Title: US-09-529-206E-26
Perfect score: 78
Sequence: 1 AGAARASGPGGGAPR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	78	100.0	180	1	US-08-791-495-9	Sequence 9, Appli
2	78	100.0	180	2	US-08-937-263B-8	Sequence 8, Appli
3	78	100.0	180	2	US-09-751-798-8	Sequence 8, Appli
4	78	100.0	180	2	US-09-392-714-25	Sequence 25, Appl
5	78	100.0	180	2	US-09-165-546D-15	Sequence 15, Appl
6	78	100.0	180	2	US-09-341-829A-9	Sequence 9, Appli
7	78	100.0	180	2	US-09-849-602-30	Sequence 30, Appl
8	70	89.7	180	1	US-08-791-495-7	Sequence 7, Appli
9	70	89.7	180	2	US-09-341-829A-7	Sequence 7, Appli
10	70	89.7	210	1	US-08-791-495-5	Sequence 5, Appli
11	70	89.7	210	2	US-09-341-829A-5	Sequence 5, Appli
12	58	74.4	456	2	US-09-252-991A-17335	Sequence 17335, A
13	56	71.8	210	2	US-09-252-991A-24923	Sequence 24923, A
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15	50	64.1	366	2	US-09-902-540-13196	Sequence 13196, A
16	50	64.1	421	2	US-09-252-991A-32326	Sequence 32326, A
17	49.5	63.5	836	2	US-09-491-356C-21	Sequence 21, Appl
18	49	62.8	143	2	US-08-789-329C-10	Sequence 10, Appl
19	49	62.8	172	2	US-08-789-329C-7	Sequence 7, Appli
20	49	62.8	175	2	US-08-789-329C-3	Sequence 3, Appli
21	49	62.8	416	2	US-09-252-991A-30219	Sequence 30219, A
22	48	61.5	9	2	US-09-344-040C-117	Sequence 117, App
23	48	61.5	9	2	US-09-833-039A-117	Sequence 117, App
24	48	61.5	196	2	US-09-252-991A-30527	Sequence 30527, A
25	48	61.5	329	2	US-09-252-991A-19752	Sequence 19752, A
26	48	61.5	370	2	US-09-252-991A-23998	Sequence 23998, A
27	48	61.5	809	2	US-09-252-991A-31759	Sequence 31759, A
28	48	61.5	1427	2	US-09-252-991A-20577	Sequence 20577, A
29	47.5	60.9	268	2	US-09-252-991A-31279	Sequence 31279, A
30	47.5	60.9	678	2	US-10-104-047-3295	Sequence 3295, Ap
31	47	60.3	134	2	US-09-252-991A-19800	Sequence 19800, A
32	47	60.3	166	2	US-09-252-991A-20512	Sequence 20512, A
33	47	60.3	214	2	US-09-852-100B-5	Sequence 5, Appli
34	47	60.3	624	2	US-09-417-197-57	Sequence 57, Appl
35	47	60.3	849	2	US-09-252-991A-21865	Sequence 21865, A
36	46	59.0	480	2	US-09-252-991A-20125	Sequence 20125, A
37	46	59.0	608	2	US-09-464-377-2	Sequence 2, Appli
38	46	59.0	608	2	US-09-464-377-3	Sequence 3, Appli
39	46	59.0	789	2	US-09-252-991A-25611	Sequence 25611, A
40	46	59.0	974	2	US-08-938-291A-4	Sequence 4, Appli
41	46	59.0	974	2	US-09-589-619-4	Sequence 4, Appli
42	45	57.7	47	1	US-08-425-069-26	Sequence 26, Appl
43	45	57.7	47	1	US-08-209-747-37	Sequence 37, Appl
44	45	57.7	47	1	US-08-458-298-37	Sequence 37, Appl
45	45	57.7	47	1	US-08-317-844B-26	Sequence 26, Appl

ALIGNMENTS

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RESULT 1
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL-1 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-791-495-9

  Query Match           100.0%;  Score 78;  DB 1;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.01;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
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Db         48 AGAARASGPGGGAPR 62
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RESULT 2
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
;  GENERAL INFORMATION:
;    APPLICANT:  Chen, Yao-Tseng; Scanlan, Matthew;
;    APPLICANT:  Gure, Ali; Old, Lloyd J.; Jager, Elke;
;    APPLICANT:  Alexander, Knuth; Drijfhout, Jan W.
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULE
;    TITLE OF INVENTION:  ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
;    TITLE OF INVENTION:  ITSELF, AND USES THEREOF
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/937,263B
;      FILING DATE:  September 15, 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sinn, Eric, Patent Agent
;      REGISTRATION NUMBER:  40,177
;      REFERENCE/DOCKET NUMBER:  LUD 5466.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3000
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-937-263B-8

  Query Match             100.0%;  Score 78;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
;  GENERAL INFORMATION:
;    APPLICANT:  Stockert, Elisabeth; Jager, Elke;
;    APPLICANT:  Chen, Yao-tseng; Scanlan, Matthew;
;    APPLICANT:  Knuth, Alexander; Old, Lloyd J.
;    TITLE OF INVENTION:  Antibodies Which Bind to NY-ESO-1 Cancer
;    TITLE OF INVENTION:  Associated Proteins, Uses Thereof,
;    TITLE OF INVENTION:  Truncated Forms of NY-ESO-1, and HLA
;    TITLE OF INVENTION:  Binding Peptides Derived Therefrom
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/751,798
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/062,422
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 6525177man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3168
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-09-751-798-8

  Query Match             100.0%;  Score 78;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 4
US-09-392-714-25
; Sequence 25, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT: Gure, Ali O.
;  APPLICANT: Williamson, Barbara
;  APPLICANT: Chen, Yao-Tseng
;  APPLICANT: Old, Lloyd J.
;  TITLE OF INVENTION: Cancer Associated Antigens and Uses
;  TITLE OF INVENTION: Therefor
;  FILE REFERENCE: L0461/7062
;  CURRENT APPLICATION NUMBER: US/09/392,714A
;  CURRENT FILING DATE: 1999-09-09
;  EARLIER APPLICATION NUMBER: PCT/US98/14679
;  EARLIER FILING DATE: 1998-07-15
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-392-714-25

  Query Match             100.0%;  Score 78;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
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Db         48 AGAARASGPGGGAPR 62
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RESULT 5
US-09-165-546D-15
; Sequence 15, Application US/09165546D
; Patent No. 6723832
;   GENERAL INFORMATION:
;        APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
;                   Gure, Ali, Old, Lloyd, Ritter, Gerd
;        TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                            SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
;                            USES THEREOF
;        NUMBER OF SEQUENCES: 15
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FULBRIGHT & JAWORSKI LLP
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10158
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/165,546D
;             FILING DATE: 02-Oct-1998
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: April 17, 1998
;             APPLICATION NUMBER: 08/937,263
;             FILING DATE: September 15, 1997
;             APPLICATION NUMBER: US 08/725,182
;             FILING DATE: October 3, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, No. 6723832man D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3000
;             TELEFAX: (212) 318-3400
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 180 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15

  Query Match             100.0%;  Score 78;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 6
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-9

  Query Match             100.0%;  Score 78;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 7
US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT:  Old, Lloyd J.
;  APPLICANT:  Stockert, Elisabeth
;  APPLICANT:  Chen, Yao-Tseng
;  TITLE OF INVENTION: Colon Cancer Antigen Panel
;  FILE REFERENCE: L0461/7105(JRV)
;  CURRENT APPLICATION NUMBER: US/09/849,602
;  CURRENT FILING DATE:  2001-05-04
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-849-602-30

  Query Match             100.0%;  Score 78;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
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Db         48 AGAARASGPGGGAPR 62


RESULT 8
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL-1 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-791-495-7

  Query Match             89.7%;  Score 70;  DB 1;  Length 180;
  Best Local Similarity   93.3%;  Pred. No. 0.098;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              ||||||||| |||||
Db         48 AGAARASGPRGGAPR 62


RESULT 9
US-09-341-829A-7
; Sequence 7, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-7

  Query Match             89.7%;  Score 70;  DB 2;  Length 180;
  Best Local Similarity   93.3%;  Pred. No. 0.098;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              ||||||||| |||||
Db         48 AGAARASGPRGGAPR 62


RESULT 10
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL-1 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  210 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-791-495-5

  Query Match             89.7%;  Score 70;  DB 1;  Length 210;
  Best Local Similarity   93.3%;  Pred. No. 0.11;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              ||||||||| |||||
Db         48 AGAARASGPRGGAPR 62


RESULT 11
US-09-341-829A-5
; Sequence 5, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-5

  Query Match             89.7%;  Score 70;  DB 2;  Length 210;
  Best Local Similarity   93.3%;  Pred. No. 0.11;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              ||||||||| |||||
Db         48 AGAARASGPRGGAPR 62


RESULT 12
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US-09-252-991A-17335
; Sequence 17335, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17335
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17335

Query Match 74.4%; Score 58; DB 2; Length 456;
Best Local Similarity 73.3%; Pred. No. 6.8;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 AGAARASGPGGGAPR 15
              ||| ||:||| | ||
Db        277 AGAGRAAGPGTGQPR 291
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RESULT 13
US-09-252-991A-24923
; Sequence 24923, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24923
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24923

Query Match 71.8%; Score 56; DB 2; Length 210;
Best Local Similarity 73.3%; Pred. No. 6;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 AGAARASGPGGGAPR 15
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Db        156 AGTAAADGAGGGAPR 170
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RESULT 14
US-09-252-991A-17249
; Sequence 17249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17249
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17249

Query Match 64.1%; Score 50; DB 2; Length 160;
Best Local Similarity 69.2%; Pred. No. 26;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Qy          3 AARASGPGGGAPR 15
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Db        117 AGRRAGPGGSAPR 129
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RESULT 15
US-09-902-540-13196
; Sequence 13196, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13196
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13196

Query Match 64.1%; Score 50; DB 2; Length 366;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 AGAARASGPGGGAPR 15
              || | |:|||  |||
Db         72 AGTAPAAGPGATAPR 86
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Search completed: March 13, 2006, 19:18:50
Job time : 27.8824 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:51:56 ; Search time 90.7059 Seconds
(without alignments)
69.096 Million cell updates/sec

Title: US-09-529-206E-26
Perfect score: 78
Sequence: 1 AGAARASGPGGGAPR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	78	100.0	30	4	US-10-296-734-1404	Sequence 1404, Ap
2	78	100.0	179	5	US-10-482-029-202	Sequence 202, App
3	78	100.0	180	3	US-09-751-798-8	Sequence 8, Appli
4	78	100.0	180	3	US-09-849-602-30	Sequence 30, Appl
5	78	100.0	180	4	US-10-023-182-8	Sequence 8, Appli
6	78	100.0	180	4	US-10-207-655-71	Sequence 71, Appl
7	78	100.0	180	4	US-10-364-614-14	Sequence 14, Appl
8	78	100.0	180	4	US-10-026-066-3	Sequence 3, Appli
9	78	100.0	180	4	US-10-117-937-74	Sequence 74, Appl
10	78	100.0	180	4	US-10-295-027-386	Sequence 386, App
11	78	100.0	180	4	US-10-296-734-832	Sequence 832, App
12	78	100.0	180	4	US-10-188-832-139	Sequence 139, App
13	78	100.0	180	4	US-10-777-053-11	Sequence 11, Appl
14	78	100.0	180	4	US-10-751-088-15	Sequence 15, Appl
15	78	100.0	180	4	US-10-657-022-74	Sequence 74, Appl
16	78	100.0	180	4	US-10-837-217-11	Sequence 11, Appl
17	78	100.0	180	5	US-10-877-373-9	Sequence 9, Appli
18	78	100.0	180	5	US-10-723-860-1270	Sequence 1270, Ap
19	78	100.0	180	5	US-10-871-708-7	Sequence 7, Appli
20	78	100.0	180	5	US-10-895-523-3	Sequence 3, Appli
21	78	100.0	180	5	US-10-182-506A-3	Sequence 3, Appli
22	78	100.0	180	5	US-10-756-149-5024	Sequence 5024, Ap
23	78	100.0	180	6	US-11-067-064-74	Sequence 74, Appl
24	78	100.0	180	6	US-11-067-159-74	Sequence 74, Appl
25	78	100.0	397	3	US-09-821-883-27	Sequence 27, Appl
26	78	100.0	397	6	US-11-144-912-27	Sequence 27, Appl
27	78	100.0	3541	4	US-10-296-734-1454	Sequence 1454, Ap
28	70	89.7	30	4	US-10-296-734-1436	Sequence 1436, Ap
29	70	89.7	135	4	US-10-295-027-388	Sequence 388, App
30	70	89.7	135	4	US-10-188-832-141	Sequence 141, App
31	70	89.7	180	4	US-10-146-473-69	Sequence 69, Appl
32	70	89.7	180	4	US-10-117-937-75	Sequence 75, Appl
33	70	89.7	180	4	US-10-296-734-834	Sequence 834, App
34	70	89.7	180	4	US-10-468-406-4	Sequence 4, Appli
35	70	89.7	180	4	US-10-657-022-75	Sequence 75, Appl
36	70	89.7	180	5	US-10-877-373-7	Sequence 7, Appli
37	70	89.7	180	6	US-11-067-064-75	Sequence 75, Appl
38	70	89.7	180	6	US-11-067-159-75	Sequence 75, Appl
39	70	89.7	210	4	US-10-157-031-88	Sequence 88, Appl
40	70	89.7	210	4	US-10-117-937-76	Sequence 76, Appl
41	70	89.7	210	4	US-10-657-022-76	Sequence 76, Appl
42	70	89.7	210	5	US-10-877-373-5	Sequence 5, Appli
43	70	89.7	210	6	US-11-067-064-76	Sequence 76, Appl
44	70	89.7	210	6	US-11-067-159-76	Sequence 76, Appl
45	66	84.6	20	4	US-10-313-986-496	Sequence 496, App

ALIGNMENTS

RESULT 1
US-10-296-734-1404
; Sequence 1404, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1404
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSO1a segment 4
US-10-296-734-1404

Query Match 100.0%; Score 78; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAPR 15
||||||||||||||||
Db 5 AGAARASGPGGGAPR 19

RESULT 2
US-10-482-029-202
; Sequence 202, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-202

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  Query Match             100.0%;  Score 78;  DB 5;  Length 179;
  Best Local Similarity   100.0%;  Pred. No. 0.068;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. US20020010321A1
; GENERAL INFORMATION:
;    APPLICANT:  Stockert, Elisabeth; Jager, Elke;
;    APPLICANT:  Chen, Yao-tseng; Scanlan, Matthew;
;    APPLICANT:  Knuth, Alexander; Old, Lloyd J.
;    TITLE OF INVENTION:  Antibodies Which Bind to NY-ESO-1 Cancer
;    TITLE OF INVENTION:  Associated Proteins, Uses Thereof,
;    TITLE OF INVENTION:  Truncated Forms of NY-ESO-1, and HLA
;    TITLE OF INVENTION:  Binding Peptides Derived Therefrom
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/751,798
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/062,422
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. US20020010321A1man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3168
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-09-751-798-8

  Query Match             100.0%;  Score 78;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.068;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 4
US-09-849-602-30
; Sequence 30, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT:  Old, Lloyd J.
;  APPLICANT:  Stockert, Elisabeth
;  APPLICANT:  Chen, Yao-Tseng
;  TITLE OF INVENTION: Colon Cancer Antigen Panel
;  FILE REFERENCE: L0461/7105(JRV)
;  CURRENT APPLICATION NUMBER: US/09/849,602
;  CURRENT FILING DATE:  2001-05-04
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-849-602-30

  Query Match             100.0%;  Score 78;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.068;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 5
US-10-023-182-8
; Sequence 8, Application US/10023182
; Publication No. US20020164665A1
;   GENERAL INFORMATION:
;        APPLICANT: Stockert, Elisabeth; Jager, Elke;
;                   Chen, Yao-tseng; Scanlan, Matthew;
;                   Knuth, Alexander; Old, Lloyd J.
;        TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
;                            Associated Proteins, Uses Thereof,
;                            Truncated Forms of NY-ESO-1, and HLA
;                            Binding Peptides Derived Therefrom
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fulbright & Jaworski, L.L.P.
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10103
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: WordPerfect
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/023,182
;             FILING DATE: 17-Dec-2001
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/751,798
;             FILING DATE: December 29, 2000
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/725,182
;             FILING DATE: October 3, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, No. US20020164665A1man D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 5466.3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3168
;             TELEFAX: (212) 752-5958
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 180
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-023-182-8
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  Query Match           100.0%;  Score 78;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.068;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 6
US-10-207-655-71
; Sequence 71, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-207-655-71

  Query Match           100.0%;  Score 78;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.068;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 7
US-10-364-614-14
; Sequence 14, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
;  APPLICANT: JAGER, Elke
;  APPLICANT:  KNUTH, Alexander
;  APPLICANT:  OLD, Lloyd
;  APPLICANT:  Gnjatic, Sacha
;  TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
;  FILE REFERENCE: LUD 5726.1 CIP
;  CURRENT APPLICATION NUMBER: US/10/364,614
;  CURRENT FILING DATE:  2003-02-24
;  PRIOR APPLICATION NUMBER: US 60/355,828
;  PRIOR FILING DATE: 2002-02-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-364-614-14

  Query Match           100.0%;  Score 78;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.068;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 8
US-10-026-066-3
; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
; GENERAL INFORMATION:
;  APPLICANT: Simard, John J. L.
;  APPLICANT:  Diamond, David C.
;  TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
;  TITLE OF INVENTION:  PRESENTING CELLS
;  FILE REFERENCE: CTLIMM.21CP1C
;  CURRENT APPLICATION NUMBER: US/10/026,066
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: 09/561,074
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 09/560,465
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 09/561,572
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 09/561,571
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: PCT/US01/13806
;  PRIOR FILING DATE: 2001-04-27
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-026-066-3

  Query Match           100.0%;  Score 78;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.068;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 9
US-10-117-937-74
; Sequence 74, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
;  APPLICANT: CTL IMMUNO THERAPIES CORP.
;  APPLICANT:  SIMARD, John, J.L.
;  APPLICANT:  DIAMOND, David, C.
;  APPLICANT:  LIU, Liping
;  APPLICANT:  XIE, Zhidong
;  TITLE OF INVENTION: EPITOPE SEQUENCES
;  FILE REFERENCE: CTLIMM.027A
;  CURRENT APPLICATION NUMBER: US/10/117,937
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: US 60/282,211
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/337,017
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: US 60/363,210
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 602
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-117-937-74

  Query Match           100.0%;  Score 78;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.068;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 10
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US-10-295-027-386
; Sequence 386, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 386
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-386

Query Match 100.0%; Score 78; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAPR 15
||||||||||||||||
Db 48 AGAARASGPGGGAPR 62

RESULT 11
US-10-296-734-832
; Sequence 832, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 832
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYNSO1a consensus polypeptide
US-10-296-734-832

Query Match 100.0%; Score 78; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAPR 15
||||||||||||||||
Db 48 AGAARASGPGGGAPR 62

RESULT 12
US-10-188-832-139
; Sequence 139, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-139

Query Match 100.0%; Score 78; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAPR 15
||||||||||||||||
Db 48 AGAARASGPGGGAPR 62

RESULT 13
US-10-777-053-11
; Sequence 11, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANNK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07

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;  PRIOR APPLICATION NUMBER: 60/336,968
;  PRIOR FILING DATE: 2001-11-07
;  NUMBER OF SEQ ID NOS: 979
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-777-053-11

  Query Match             100.0%;  Score 78;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.068;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              ||||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 14
US-10-751-088-15
; Sequence 15, Application US/10751088
; Publication No. US20040158044A1
;   GENERAL INFORMATION:
;        APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
;                   Gure, Ali, Old, Lloyd, Ritter, Gerd
;        TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                            SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
;                            USES THEREOF
;        NUMBER OF SEQUENCES: 15
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FULBRIGHT & JAWORSKI LLP
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10158
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/751,088
;             FILING DATE: 02-Jan-2004
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/165,546D
;             FILING DATE: 02-Oct-1998
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: April 17, 1998
;             APPLICATION NUMBER: 08/937,263
;             FILING DATE: September 15, 1997
;             APPLICATION NUMBER: US 08/725,182
;             FILING DATE: October 3, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, Norman D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3000
;             TELEFAX: (212) 318-3400
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 180 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-10-751-088-15

  Query Match             100.0%;  Score 78;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.068;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              ||||||||||||||||
Db         48 AGAARASGPGGGAPR 62


RESULT 15
US-10-657-022-74
; Sequence 74, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
;  APPLICANT: Simard, John J. L.
;  APPLICANT:  Diamond, David C.
;  APPLICANT:  Liu, Liping
;  APPLICANT:  Liu, Zheng
;  TITLE OF INVENTION: EPITOPE SEQUENCES
;  FILE REFERENCE: MANNK.032A
;  CURRENT APPLICATION NUMBER: US/10/657,022
;  CURRENT FILING DATE:  2003-09-04
;  PRIOR APPLICATION NUMBER: 60/409123
;  PRIOR FILING DATE: 2002-09-06
;  NUMBER OF SEQ ID NOS: 610
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-657-022-74

  Query Match             100.0%;  Score 78;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.068;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              ||||||||||||||||
Db         48 AGAARASGPGGGAPR 62


Search completed: March 13, 2006, 20:02:26
Job time : 90.7059 secs
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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:54:06 ; Search time 10.2353 Seconds
(without alignments)
40.793 Million cell updates/sec

Title: US-09-529-206E-26
Perfect score: 78
Sequence: 1 AGAARASGPGGGAPR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	78	100.0	180	7	US-11-155-288-7	Sequence 7, Appli
2	78	100.0	240	7	US-11-021-441-28	Sequence 28, Appl
3	66	84.6	20	6	US-10-623-155-496	Sequence 496, App
4	53	67.9	306	7	US-11-096-568A-20556	Sequence 20556, A
5	53	67.9	353	7	US-11-096-568A-22334	Sequence 22334, A
6	53	67.9	358	7	US-11-096-568A-22333	Sequence 22333, A
7	53	67.9	420	7	US-11-096-568A-22332	Sequence 22332, A
8	48	61.5	359	7	US-11-096-568A-22662	Sequence 22662, A
9	48	61.5	391	7	US-11-096-568A-22661	Sequence 22661, A
10	47.5	60.9	167	7	US-11-096-568A-10542	Sequence 10542, A
11	47.5	60.9	678	7	US-11-072-512-3295	Sequence 3295, Ap
12	47	60.3	214	6	US-10-892-379-5	Sequence 5, Appli
13	46	59.0	134	7	US-11-096-568A-23806	Sequence 23806, A
14	46	59.0	287	7	US-11-096-568A-25788	Sequence 25788, A
15	46	59.0	293	7	US-11-096-568A-17631	Sequence 17631, A
16	46	59.0	298	7	US-11-096-568A-25787	Sequence 25787, A
17	46	59.0	304	7	US-11-096-568A-17630	Sequence 17630, A
18	46	59.0	341	7	US-11-096-568A-25786	Sequence 25786, A
19	46	59.0	360	7	US-11-129-143-113	Sequence 113, App
20	46	59.0	608	7	US-11-241-347-8	Sequence 8, Appli
21	46	59.0	974	6	US-10-531-036-35	Sequence 35, Appl
22	45.5	58.3	280	7	US-11-143-980-34	Sequence 34, Appl
23	45	57.7	31	7	US-11-145-861-426	Sequence 426, App
24	45	57.7	32	7	US-11-145-861-407	Sequence 407, App
25	45	57.7	119	7	US-11-110-424-4	Sequence 4, Appli
26	45	57.7	268	7	US-11-087-099-6009	Sequence 6009, Ap
27	45	57.7	413	7	US-11-096-568A-27265	Sequence 27265, A
28	45	57.7	441	7	US-11-087-099-3243	Sequence 3243, Ap
29	45	57.7	830	6	US-10-921-793-38	Sequence 38, Appl
30	45	57.7	830	6	US-10-931-198-38	Sequence 38, Appl
31	44	56.4	256	7	US-11-186-284-65	Sequence 65, Appl
32	44	56.4	298	6	US-10-821-234-1240	Sequence 1240, Ap
33	44	56.4	361	7	US-11-129-143-108	Sequence 108, App
34	44	56.4	368	7	US-11-129-143-107	Sequence 107, App
35	44	56.4	379	7	US-11-109-156-16	Sequence 16, Appl
36	44	56.4	532	7	US-11-096-568A-22026	Sequence 22026, A
37	44	56.4	558	7	US-11-096-568A-26217	Sequence 26217, A
38	43	55.1	101	7	US-11-096-568A-14205	Sequence 14205, A
39	43	55.1	102	7	US-11-096-568A-24201	Sequence 24201, A
40	43	55.1	113	7	US-11-096-568A-8816	Sequence 8816, Ap
41	43	55.1	135	7	US-11-096-568A-14203	Sequence 14203, A
42	43	55.1	155	7	US-11-096-568A-19104	Sequence 19104, A
43	43	55.1	280	7	US-11-052-554A-318	Sequence 318, App
44	43	55.1	306	7	US-11-096-568A-19986	Sequence 19986, A
45	43	55.1	307	7	US-11-096-568A-19985	Sequence 19985, A

ALIGNMENTS

RESULT 1
US-11-155-288-7
; Sequence 7, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-7

Query Match 100.0%; Score 78; DB 7; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAPR 15
||||||||||||||||
Db 48 AGAARASGPGGGAPR 62

RESULT 2
US-11-021-441-28
; Sequence 28, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06

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;  PRIOR APPLICATION NUMBER: US 60/615,287
;  PRIOR FILING DATE: 2004-10-01
;  PRIOR APPLICATION NUMBER: US 60/599,377
;  PRIOR FILING DATE: 2004-08-05
;  PRIOR APPLICATION NUMBER: PCT/US2004/23881
;  PRIOR FILING DATE: 2004-07-23
;  PRIOR APPLICATION NUMBER: US 10/883,599
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: US 60/556,744
;  PRIOR FILING DATE: 2004-03-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion protein
US-11-021-441-28

  Query Match             100.0%;  Score 78;  DB 7;  Length 240;
  Best Local Similarity   100.0%;  Pred. No. 0.0017;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGAPR 15
              |||||||||||||||
Db        108 AGAARASGPGGGAPR 122


RESULT 3
US-10-623-155-496
; Sequence 496, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Peckham, David W.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C20
;  CURRENT APPLICATION NUMBER: US/10/623,155
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 496
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-623-155-496

  Query Match             84.6%;  Score 66;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.0065;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGA 13
              |||||||||||||
Db          8 AGAARASGPGGGA 20


RESULT 4
US-11-096-568A-20556
; Sequence 20556, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20556
;   LENGTH: 306
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(306)
;   OTHER INFORMATION: Ceres Seq. ID no. 12383286
US-11-096-568A-20556

  Query Match             67.9%;  Score 53;  DB 7;  Length 306;
  Best Local Similarity   76.9%;  Pred. No. 3.3;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 GAARASGPGGGAP 14
              | ||| ||| |||
Db         89 GVARADGPGTGAP 101


RESULT 5
US-11-096-568A-22334
; Sequence 22334, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22334
;   LENGTH: 353
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(353)
;   OTHER INFORMATION: Ceres Seq. ID no. 12408544
US-11-096-568A-22334

  Query Match             67.9%;  Score 53;  DB 7;  Length 353;
  Best Local Similarity   71.4%;  Pred. No. 3.8;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 GAARASGPGGGAPR 15
              ||||  ||||  ||
Db        107 GAARGQGPGGEQPR 120


RESULT 6
US-11-096-568A-22333
; Sequence 22333, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22333
;   LENGTH: 358
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(358)
;   OTHER INFORMATION: Ceres Seq. ID no. 12408543
US-11-096-568A-22333

  Query Match             67.9%;  Score 53;  DB 7;  Length 358;
  Best Local Similarity   71.4%;  Pred. No. 3.8;
```

```
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 GAARASGPGGGAPR 15
              ||||  ||||  ||
Db        112 GAARGQGPGGEQPR 125


RESULT 7
US-11-096-568A-22332
; Sequence 22332, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22332
;   LENGTH: 420
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(420)
;   OTHER INFORMATION: Ceres Seq. ID no. 12408542
US-11-096-568A-22332

  Query Match             67.9%;  Score 53;  DB 7;  Length 420;
  Best Local Similarity   71.4%;  Pred. No. 4.4;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 GAARASGPGGGAPR 15
              ||||  ||||  ||
Db        174 GAARGQGPGGEQPR 187


RESULT 8
US-11-096-568A-22662
; Sequence 22662, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22662
;   LENGTH: 359
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(359)
;   OTHER INFORMATION: Ceres Seq. ID no. 12409619
US-11-096-568A-22662

  Query Match             61.5%;  Score 48;  DB 7;  Length 359;
  Best Local Similarity   68.8%;  Pred. No. 17;
  Matches   11;  Conservative    1;  Mismatches    2;  Indels    2;  Gaps    1;

Qy          1 AGAARASGPG--GGAP 14
              |||||  :||   ||||
Db         34 AGAARRAGPSAPGGAP 49


RESULT 9
US-11-096-568A-22661
; Sequence 22661, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22661
;   LENGTH: 391
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(391)
;   OTHER INFORMATION: Ceres Seq. ID no. 12409618
US-11-096-568A-22661

  Query Match             61.5%;  Score 48;  DB 7;  Length 391;
  Best Local Similarity   68.8%;  Pred. No. 18;
  Matches   11;  Conservative    1;  Mismatches    2;  Indels    2;  Gaps    1;

Qy          1 AGAARASGPG--GGAP 14
              |||||  :||   ||||
Db         66 AGAARRAGPSAPGGAP 81


RESULT 10
US-11-096-568A-10542
; Sequence 10542, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 10542
;   LENGTH: 167
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(167)
;   OTHER INFORMATION: Ceres Seq. ID no. 13596390
US-11-096-568A-10542

  Query Match             60.9%;  Score 47.5;  DB 7;  Length 167;
  Best Local Similarity   73.3%;  Pred. No. 9.9;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          2 GAARASGP-GGGAPR 15
              |||   || ||||||
Db         92 GAAPGRGPRGGGAPR 106


RESULT 11
US-11-072-512-3295
; Sequence 3295, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
;  APPLICANT: ISOGAI, TAKAO
;  APPLICANT:  SUGIYAMA, TOMOYASU
;  APPLICANT:  OTSUKI, TETSUJI
;  APPLICANT:  WAKAMATSU, AI
;  APPLICANT:  SATO, HIROYUKI
;  APPLICANT:  ISHII, SHIZUKO
;  APPLICANT:  YAMAMOTO, JUN-ICHI
;  APPLICANT:  ISONO, YUUKO
;  APPLICANT:  HIO, YURI
;  APPLICANT:  OTSUKA, KAORU
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;  APPLICANT:  NAGAI, KEIICHI
;  APPLICANT:  IRIE, RYOTARO
;  APPLICANT:  TAMECHIKA, ICHIRO
;  APPLICANT:  SEKI, NAOHIKO
;  APPLICANT:  YOSHIKAWA, TSUTOMU
;  APPLICANT:  OTSUKA, MOTOYUKI
;  APPLICANT:  NAGAHARI, KENJI
;  APPLICANT:  MASUHO, YASUHIKO
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: 084335-0191
;  CURRENT APPLICATION NUMBER: US/11/072,512
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: US 60/350,978
;  PRIOR FILING DATE: 2002-01-25
;  PRIOR APPLICATION NUMBER: JP 2001-379298
;  PRIOR FILING DATE: 2001-11-05
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3295
;   LENGTH: 678
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-072-512-3295

  Query Match            60.9%;  Score 47.5;  DB 7;  Length 678;
  Best Local Similarity   48.0%;  Pred. No. 34;
  Matches   12;  Conservative    1;  Mismatches    1;  Indels   11;  Gaps    1;

Qy          1 AGAA----------RASGPGGGAP 14
              ||||          ||:||||| |
Db        577 AGAARPEGAAKPPRPRAAGPGGGWP 601


RESULT 12
US-10-892-379-5
; Sequence 5, Application US/10892379
; Publication No. US20050282999A9
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Ozenberger, Bradley  A.
;  APPLICANT:  Bard, Jonathan A.
;  APPLICANT:  Kajkowski, Eileen M.
;  APPLICANT:  Jacobsen, Jack S.
;  APPLICANT:  Walker, Stephen G.
;  APPLICANT:  Sophia, Heidi
;  APPLICANT:  Howland, David
;  TITLE OF INVENTION: Beta-Amyloid Peptide-Binding Proteins and Polynucleotides
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: 31896-67300 (AHP98126P2 C1)
;  CURRENT APPLICATION NUMBER: US/10/892,379
;  CURRENT FILING DATE:  2004-07-16
;  PRIOR APPLICATION NUMBER: 09/852,100
;  PRIOR FILING DATE: 2001-05-09
;  PRIOR APPLICATION NUMBER: US 09/774,936
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: US 09/172,990
;  PRIOR FILING DATE: 1998-10-14
;  PRIOR APPLICATION NUMBER: US 09/060,609
;  PRIOR FILING DATE: 1998-04-15
;  PRIOR APPLICATION NUMBER: US 60/064,583
;  PRIOR FILING DATE: 1997-04-16
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-892-379-5

  Query Match            60.3%;  Score 47;  DB 6;  Length 214;
  Best Local Similarity   69.2%;  Pred. No. 14;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGGA 13
              ||||:  |||| |
Db         47 AGAAQPEGPGGAA 59


RESULT 13
US-11-096-568A-23806
; Sequence 23806, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23806
;   LENGTH: 134
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(134)
;   OTHER INFORMATION: Ceres Seq. ID no. 12415289
US-11-096-568A-23806

  Query Match            59.0%;  Score 46;  DB 7;  Length 134;
  Best Local Similarity   72.7%;  Pred. No. 13;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 ARASGPGGGAP 14
              || :||| |||
Db         69 ARGAGPGAGAP 79


RESULT 14
US-11-096-568A-25788
; Sequence 25788, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 25788
;   LENGTH: 287
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(287)
;   OTHER INFORMATION: Ceres Seq. ID no. 13493532
US-11-096-568A-25788

  Query Match            59.0%;  Score 46;  DB 7;  Length 287;
  Best Local Similarity   75.0%;  Pred. No. 25;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGG 12
              |||| | || ||
Db         76 AGAAAAGGPSGG 87


RESULT 15
US-11-096-568A-17631
; Sequence 17631, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
```

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;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17631
;   LENGTH: 293
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(293)
;   OTHER INFORMATION: Ceres Seq. ID no. 12359516
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (6)..(6)
;   OTHER INFORMATION: Xaa is any aa, unknown or other
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (77)..(77)
;   OTHER INFORMATION: Xaa is any aa, unknown or other
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (78)..(78)
;   OTHER INFORMATION: Xaa is any aa, unknown or other
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (79)..(79)
;   OTHER INFORMATION: Xaa is any aa, unknown or other
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (81)..(81)
;   OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-17631

  Query Match           59.0%;  Score 46;  DB 7;  Length 293;
  Best Local Similarity  75.0%;  Pred. No. 25;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AGAARASGPGGG 12
              |||| | || ||
Db         82 AGAAAAGGPSGG 93


Search completed: March 13, 2006, 20:03:30
Job time : 10.2353 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 18:52:59 ; Search time 105.412 Seconds
(without alignments)
58.355 Million cell updates/sec

Title: US-09-529-206E-27
Perfect score: 74
Sequence: 1 GAARASGPGGGAPR 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	74	100.0	14	2	AAY05986	Aay05986 Human can
2	74	100.0	15	2	AAY05978	Aay05978 Human can
3	74	100.0	20	2	AAY05979	Aay05979 Human can
4	74	100.0	30	5	AAU85105	Aau85105 Human NYN
5	74	100.0	179	8	ADK68648	Adk68648 Epitope 1
6	74	100.0	180	2	AAW62584	Aaw62584 Cancer as
7	74	100.0	180	2	AAW69665	Aaw69665 Human NY-
8	74	100.0	180	2	AAY05965	Aay05965 Human can
9	74	100.0	180	3	AAY52430	Aay52430 Human tum
10	74	100.0	180	3	AAY70862	Aay70862 Human tum
11	74	100.0	180	3	AAB03154	Aab03154 Human oes
12	74	100.0	180	4	AAB69946	Aab69946 Human NY-
13	74	100.0	180	4	AAG67164	Aag67164 Amino aci
14	74	100.0	180	4	AAU01535	Aau01535 Human NY-
15	74	100.0	180	4	AAE07714	Aae07714 Human NY
16	74	100.0	180	5	AAU84818	Aau84818 Human NYN
17	74	100.0	180	5	AAU11543	Aau11543 Human tum
18	74	100.0	180	6	ABR58672	Abr58672 Human can
19	74	100.0	180	6	ABR48210	Abr48210 Human bla
20	74	100.0	180	6	ABU56508	Abu56508 Lung canc
21	74	100.0	180	6	ABU56694	Abu56694 Lung canc
22	74	100.0	180	6	ABP74198	Abp74198 Human NY-
23	74	100.0	180	6	ABU64816	Abu64816 Human NY-
24	74	100.0	180	6	ABR83438	Abr83438 Human NY-
25	74	100.0	180	7	ADC09576	Adc09576 NY-ESO-1
26	74	100.0	180	7	ADD35564	Add35564 Human NY-
27	74	100.0	180	7	ADD35568	Add35568 Human NY-
28	74	100.0	180	7	ADD25510	Add25510 Binding d
29	74	100.0	180	7	ADN39068	Adn39068 Cancer/an
30	74	100.0	180	8	ADJ54139	Adj54139 Human NY-
31	74	100.0	180	8	ADM72815	Adm72815 Human NY-
32	74	100.0	180	8	ADM73418	Adm73418 CAG-3 pro
33	74	100.0	180	8	ADM73417	Adm73417 Human NY-
34	74	100.0	180	8	ADQ18451	Adq18451 Human sof
35	74	100.0	180	8	ADQ10446	Adq10446 Autoimmun
36	74	100.0	180	8	ADS80926	Ads80926 Tumour as
37	74	100.0	180	9	ADW44353	Adw44353 Human aut
38	74	100.0	180	9	ADY85096	Ady85096 Tumor ant
39	74	100.0	180	9	ADZ28913	Adz28913 NY-ESO-1
40	74	100.0	180	9	ADZ42374	Adz42374 Immunogen
41	74	100.0	180	9	AEA35651	Aea35651 Human NY-
42	74	100.0	240	9	ADW99402	Adw99402 NY-ESO-1/
43	74	100.0	240	9	AEB80047	Aeb80047 Human NY-
44	74	100.0	397	4	AAE13122	Aae13122 NY-ESO-IC
45	74	100.0	3541	5	AAU85130	Aau85130 Human mel

ALIGNMENTS

RESULT 1
AAY05986
ID AAY05986 standard; peptide; 14 AA.
XX
AC AAY05986;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Claim 25; Page 50; 88pp; English.
XX
CC The present sequence represents a cancer peptide that corresponds to
CC amino acid residues 49-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
CC AAY05965), a new and potent tumour antigen capable of eliciting an
CC antigen specific immune response by T cells. Cancer peptides derived from
CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
CC variants (see AAY05967-87), are useful as cancer vaccines that protect
CC against cancer. The invention provides: vectors and host cells (also
CC useful as vaccines); a method of diagnosis of cancer or precancer; a
CC transgenic animal; antisense oligonucleotides that inhibit expression of

CC the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
CC cancer peptide, useful in diagnostic and detection assays; and methods
CC for preventing or inhibiting cancer by administering a cancer peptide,
CC with or without an HLA molecule. The cancer peptides form part of, or are
CC derived from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
CC treated by inducing cancer-specific T cells in vitro for subsequent
CC return to a patient
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 74; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGGAPR 14
||||||||||||||
Db 1 GAARASGPGGGAPR 14

RESULT 2
AAY05978
ID AAY05978 standard; peptide; 15 AA.
XX
AC AAY05978;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Claim 15; Page 64; 88pp; English.
XX
CC The present sequence represents a cancer peptide that corresponds to
CC amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
CC AAY05965), a new and potent tumour antigen capable of eliciting an
CC antigen specific immune response by T cells. Cancer peptides derived from
CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
CC variants (see AAY05967-87), are useful as cancer vaccines that protect
CC against cancer. The invention provides: vectors and host cells (also
CC useful as vaccines); a method of diagnosis of cancer or precancer; a
CC transgenic animal; antisense oligonucleotides that inhibit expression of
CC the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
CC cancer peptide, useful in diagnostic and detection assays; and methods
CC for preventing or inhibiting cancer by administering a cancer peptide,
CC with or without an HLA molecule. The cancer peptides form part of, or are
CC derived from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
CC treated by inducing cancer-specific T cells in vitro for subsequent
CC return to a patient
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGGAPR 14
||||||||||||||
Db 2 GAARASGPGGGAPR 15

RESULT 3
AAY05979
ID AAY05979 standard; peptide; 20 AA.
XX
AC AAY05979;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Claim 16; Page 64; 88pp; English.
XX
CC The present sequence represents a cancer peptide that is based on amino
CC acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965),
CC a new and potent tumour antigen capable of eliciting an antigen specific
CC immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-
CC 3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-
CC 87), are useful as cancer vaccines that protect against cancer. The
CC invention provides: vectors and host cells (also useful as vaccines); a
CC method of diagnosis of cancer or precancer; a transgenic animal;
CC antisense oligonucleotides that inhibit expression of the cancer peptide
CC or tumour antigen; antibodies reacting with a CAG-3 cancer peptide,
CC useful in diagnostic and detection assays; and methods for preventing or
CC inhibiting cancer by administering a cancer peptide, with or without an
CC HLA molecule. The cancer peptides form part of, or are derived from,
CC cancers such as primary or metastatic melanoma, thymoma, lymphoma,
CC sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
CC cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,

```
CC   prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by
CC   inducing cancer-specific T cells in vitro for subsequent return to a
CC   patient
XX
SQ   Sequence 20 AA;

  Query Match             100.0%;  Score 74;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.0071;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db          7 GAARASGPGGGAPR 20


RESULT 4
AAU85105
ID   AAU85105 standard; peptide; 30 AA.
XX
AC   AAU85105;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Human NYNSO1a segment 4.
XX
KW   Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW   viral infection; human immunodeficieny virus; melanoma;
KW   bacterial infection; Salmonella; Legionella; parasitic infection;
KW   Trypanosoma; Toxoplasma; Giardia.
XX
OS   Homo sapiens.
XX
PN   WO200190197-A1.
XX
PD   29-NOV-2001.
XX
PF   25-MAY-2001; 2001WO-AU000622.
XX
PR   26-MAY-2000; 2000AU-00007761.
XX
PA   (AUSU ) UNIV AUSTRALIAN NAT.
XX
PI   Thomson SA,  Ramshaw IA;
XX
DR   WPI; 2002-147575/19.
DR   N-PSDB; ABK36925.
XX
PT   New synthetic polypeptides having several different segments of at least
PT   one parent polypeptide linked together differently compared to the
PT   linkage in the parent polypeptide, for inducing immune response against a
PT   pathogen or cancer.
XX
PS   Example 3; Fig 27; 364pp; English.
XX
CC   The invention relates to a new synthetic polypeptide (I) comprising
CC   several different segments of at least one parent polypeptide linked
CC   together in a different relationship relative to their linkage in the
CC   parent polypeptide to impede, abrogate or otherwise alter at least one
CC   function associated with the parent polypeptide and for inducing an
CC   immune response against a pathogen or cancer. Also included are a
CC   synthetic polynucleotide encoding and a computer system for designing the
CC   synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC   are referred to as a Savine. The synthetic polypeptide is useful for
CC   modulating immune responses preferably directed against a pathogen or a
CC   cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC   and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC   oesophagus, brain, testicle, uterus), as potentiating agents.
CC   Compositions comprising the polypeptide may be used in the treatment or
CC   prophylaxis against viral (such as infections caused by HIV (human
CC   immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC   virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC   (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC   Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC   (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC   Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC   a peptide derived from a parent protein used to construct a savine of the
CC   invention
XX
SQ   Sequence 30 AA;

  Query Match             100.0%;  Score 74;  DB 5;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.01;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db          6 GAARASGPGGGAPR 19


RESULT 5
ADK68648
ID   ADK68648 standard; protein; 179 AA.
XX
AC   ADK68648;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Epitope liberation-related NY-ESO-1 protein SeqID11.
XX
KW   epitope liberation; substrate; proteasome; cytostatic; antibacterial;
KW   protozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope;
KW   cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;
KW   virus; bacterium; protozoan; fungus; housekeeping proteasome system;
KW   human.
XX
OS   Homo sapiens.
XX
PN   US2003228634-A1.
XX
PD   11-DEC-2003.
XX
PF   07-NOV-2002; 2002US-00292413.
XX
PR   07-NOV-2001; 2001US-0336968P.
XX
PA   (SIMA/) SIMARD J J L.
PA   (DIAM/) DIAMOND D C.
PA   (QIUZ/) QIU Z.
PA   (LEIX/) LEI X.
XX
PI   Simard JJL,  Diamond DC,  Qiu Z,  Lei X;
XX
DR   WPI; 2004-167209/16.
DR   N-PSDB; ADK68674.
XX
PT   Identifying polypeptide suitable for epitope e.g., housekeeping epitope,
PT   liberation by contacting substrate polypeptide comprising epitope of
PT   interest, with proteasome, and assaying for liberation of epitope.
XX
PS   Example 2; SEQ ID NO 11; 67pp; English.
XX
CC   This invention relates to a novel method of identifying a polypeptide
CC   suitable for epitope liberation, including the steps of identifying an
CC   epitope of interest; providing substrate polypeptide sequence including
CC   the epitope, wherein the substrate permits processing by a proteasome;
CC   contacting the substrate with a composition including the proteasome,
CC   under conditions that support processing of the substrate by proteasome;
CC   and assaying for liberation of epitope. The invention may be useful for
CC   the development of compounds with a cytostatic, antibacterial,
CC   protozoacide or fungicide activity acting as T-cell activators. In
CC   addition, the invention may allow development of a vaccine. The invention
CC   is useful for identifying a polypeptide suitable for epitope liberation,
CC   where the epitope is a housekeeping epitope. The compositions comprising
CC   the identified housekeeping epitopes are useful in vitro in vaccine
CC   development or in the generation or expansion of cytotoxic T lymphocyte
CC   (CTL) to be used in adoptive immunotherapy. The invention is also useful
```

CC for activating T-cells against neoplastic cells, and cells infected with
CC virus, bacterium, protozoan or fungus. CTL epitopes are identified based
CC on the knowledge that such epitopes are, in fact, produced by the
CC housekeeping proteasome system. Once identified, these epitopes, embodied
CC as peptides, can be used to successfully immunise or induce therapeutic
CC CTL responses against housekeeping proteasome expressing target cells in
CC the host. The present sequence is that of a protein which is related to
CC the method of the invention.
XX
SQ Sequence 179 AA;

Query Match 100.0%; Score 74; DB 8; Length 179;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGGAPR 14
||||||||||||||
Db 48 GAARASGPGGGAPR 61

RESULT 6
AAW62584
ID AAW62584 standard; protein; 180 AA.
XX
AC AAW62584;
XX
DT 17-SEP-1998 (first entry)
XX
DE Cancer associated antigen NY-ESO-1.
XX
KW Cancer associated antigen; NY-ESO-1; regression; progression; onset;
KW cancer; treatment; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 7
FT /note= "potential myristorylation site"
FT Misc-difference 9
FT /note= "potential myristorylation site"
FT Misc-difference 11
FT /note= "potential phosphorylation site"
FT Misc-difference 98
FT /note= "potential phosphorylation site"
FT Misc-difference 134
FT /note= "potential phosphorylation site"
FT Misc-difference 138
FT /note= "potential phosphorylation site"
XX
PN WO9814464-A1.
XX
PD 09-APR-1998.
XX
PF 15-SEP-1997; 97WO-US016335.
XX
PR 03-OCT-1996; 96US-00725182.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Chen Y, Scanlan M, Gure A, Old LJ, Jager E, Knuth A;
PI Drijfhout JW;
XX
DR WPI; 1998-286417/25.
DR N-PSDB; AAV38566.
XX
PT New isolated cancer associated antigen - is used to develop products for
PT the diagnosis and treatment of cancers and for monitoring cancer therapy.
XX
PS Claim 8; Fig 3; 49pp; English.
XX
CC The present sequence represents a cancer associated antigen. The clone
CC from which the DNA sequence is obtained is designated NY-ESO-1. The
CC specification described a method for determining regression, progression
CC of onset of a cancerous condition, comprising monitoring a sample from a
CC patient with the cancerous condition for a parameter selected from NY-ESO
CC -1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells
CC specific for the peptide and an MHC molecule with which it non-covalently
CC complexes. Methods for the treatment of a cancerous condition are also
CC described. The NY-ESO-1 protein and peptides derived from it can be used
CC for diagnosis and treatment of cancers and to monitor the efficacy of a
CC therapeutic regime
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 74; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGGAPR 14
||||||||||||||
Db 49 GAARASGPGGGAPR 62

RESULT 7
AAW69665
ID AAW69665 standard; protein; 180 AA.
XX
AC AAW69665;
XX
DT 27-OCT-1998 (first entry)
XX
DE Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
XX
KW Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
XX
OS Homo sapiens.
XX
PN WO9832855-A1.
XX
PD 30-JUL-1998.
XX
PF 27-JAN-1998; 98WO-US001445.
XX
PR 27-JAN-1997; 97US-00791495.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Lethe B, Lucas S, De Smet C, Godelaine D, Boon-Falleur T;
XX
DR WPI; 1998-427951/36.
DR N-PSDB; AAV50348.
XX
PT New isolated LAGE-1 tumour associated nucleic acids - used to develop
PT products for the diagnosis and treatment of LAGE-1 associated disorders,
PT particularly tumours.
XX
PS Example 2; Page 57-58; 73pp; English.
XX
CC The present sequence represents human NY-ESO-1, formerly known as LL-1.2
CC clone, which is used in an example from the present invention which
CC describes LAGE-1 tumour associated protein (TAP). The present invention
CC also describes: (1) a method for treating a subject with a disorder
CC characterised by expression of a LAGE-1 nucleic acid molecule or an
CC expression product, comprising administering to the subject autologous
CC cytolytic T cells to ameliorate the disorder, where the cytolytic T cells
CC are specific for complexes of an HLA molecule and a LAGE-1 TAP or an
CC immunogenic fragment; (2) a method for treating a subject with a disorder
CC characterised by expression of a LAGE-1 nucleic acid molecule or an
CC expression product, comprising administering a LAGE-1 TAP or an
CC immunogenic fragment to ameliorate the disorder; and (3) a method for
CC selectively enriching a population of T cells with cytolytic T cells
CC specific for a LAGE-1 TAP comprising contacting an isolated population of
CC T cells with an agent presenting a complex of a LAGE TAP or an
CC immunogenic fragment and a HLA presenting molecule to selectively enrich
CC the isolated population of T cells with the cytolytic T cells. The
CC methods and products from the present invention can be used for the

```
CC   diagnosis and treatment of LAGE-1 associated disorders, particularly
CC   tumours
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 74;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.052;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 8
AAY05965
ID   AAY05965 standard; protein; 180 AA.
XX
AC   AAY05965;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.
XX
KW   NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia;
KW   non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis;
KW   melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer;
KW   breast cancer; prostate cancer; ovarian cancer; cervical cancer;
KW   bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma;
KW   tumour; diagnosis; immunotherapy; therapy; vaccine; ORF1.
XX
OS   Homo sapiens.
XX
PN   WO9918206-A2.
XX
PD   15-APR-1999.
XX
PF   21-SEP-1998;   98WO-US019609.
XX
PR   08-OCT-1997;   97US-0061428P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang RF,  Rosenberg SA;
XX
DR   WPI; 1999-277270/23.
DR   N-PSDB; AAX58599.
XX
PT   Cancer antigen NY ESO1/CAG-3.
XX
PS   Claim 4; Fig 3A; 88pp; English.
XX
CC   The present sequence represents the ORF1 protein encoded by open reading
CC   frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and
CC   potent tumour antigen capable of eliciting an antigen specific immune
CC   response by T cells. Cancer peptides comprising ORF1, ORF2 (see
CC   AAY05966), portions of these peptides and their variants (see AAY05965-
CC   87), are useful as cancer vaccines that protect the recipient from
CC   development of cancer. The invention provides: vectors and host cells
CC   (also useful as vaccines); a method of diagnosis of cancer or precancer;
CC   a transgenic animal; antisense oligonucleotides that inhibit expression
CC   of the cancer peptide or tumour antigen; antibodies reacting with the CAG
CC   -3 cancer peptide, useful in diagnostic and detection assays; and methods
CC   for preventing or inhibiting cancer by administering a cancer peptide,
CC   with or without an HLA molecule. The cancer peptides form part of, or are
CC   derived from, cancers such as primary or metastatic melanoma, thymoma,
CC   lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC   cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC   as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
CC   treated by inducing cancer-specific T cells in vitro for subsequent
CC   return to a patient
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 74;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.052;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 9
AAY52430
ID   AAY52430 standard; protein; 180 AA.
XX
AC   AAY52430;
XX
DT   21-OCT-2004  (revised)
DT   15-FEB-2000  (first entry)
XX
DE   Human tumour antigen NY-ESO-1.
XX
KW   Cancer; tumour; antigen; MHC; major histocompatility complex; T-cell;
KW   cytotoxic; helper; stimulation; proliferation; treatment; diagnosis;
KW   prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;
KW   hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Peptide         44. .53
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         60. .69
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         60. .68
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         63. .72
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         79. .88
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         79. .87
FT                   /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
FT                   and HLA-B35"
FT   Peptide         82. .91
FT                   /note= "Peptide presented by MHC Class I HLA-A1"
FT   Peptide         82. .90
FT                   /note= "Peptide presented by MHC Class I HLA-A1"
FT   Peptide         83. .91
FT                   /note= "Peptide presented by MHC Class I HLA-B44"
FT   Peptide         84. .92
FT                   /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
FT                   and HLA-B35"
FT   Peptide         87. .96
FT                   /note= "Peptide presented by MHC Class I HLA-A1"
FT   Peptide         88. .96
FT                   /note= "Peptide presented by MHC Class I HLA-B44"
FT   Peptide         96. .104
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         100. .108
FT                   /note= "Peptide presented by MHC Class I HLA-B44"
FT   Peptide         102. .110
FT                   /note= "Peptide presented by MHC Class I HLA-B44"
FT   Peptide         107. .116
FT                   /note= "Peptide presented by MHC Class I HLA-A24"
FT   Peptide         110. .118
FT                   /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide         113. .122
FT                   /note= "Peptide presented by MHC Class I HLA-B7 and HLA-
FT                   B52"
FT   Peptide         113. .121
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         115. .124
FT                   /note= "Peptide presented by MHC Class I HLA-A3"
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FT   Peptide         118. .126
FT                   /note= "Peptide presented by MHC Class I HLA-B35"
FT   Peptide         124. .133
FT                   /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide         125. .133
FT                   /note= "Peptide presented by MHC Class I HLA-A24"
FT   Peptide         138. .147
FT                   /note= "Peptide presented by MHC Class I HLA-B8"
FT   Peptide         139. .147
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         145. .153
FT                   /note= "Peptide presented by MHC Class I HLA-A24 and HLA-
FT                   B52"
FT   Peptide         153. .162
FT                   /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide         154. .163
FT                   /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide         154. .162
FT                   /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide         156. .167
FT                   /note= "Peptide (AAY52434) presented by MHC Class I HLA-
FT                   A2"
FT   Peptide         158. .166
FT                   /note= "Peptide presented by MHC Class I HLA-A3"
FT   Peptide         159. .167
FT                   /note= "Peptide presented by MHC Class I HLA-A3"
FT   Peptide         162. .170
FT                   /note= "Peptide presented by MHC Class I HLA-B52"
XX
PN   WO9953938-A1.
XX
PD   28-OCT-1999.
XX
PF   24-MAR-1999;   99WO-US006875.
XX
PR   17-APR-1998;   98US-00062422.
PR   02-OCT-1998;   98US-00165546.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Stockert E,  Jager E,  Chen Y,  Scanlan M,  Alexander K,  Old LJ;
PI   Gure A,  Ritter G;
XX
DR   WPI; 2000-038483/03.
DR   N-PSDB; AAZ38380.
XX
PT   Novel peptides which bind to MHC class I and MHC class II molecules,
PT   useful for therapeutic and diagnostic purposes.
XX
PS   Claim 30; Fig 3; 49pp; English.
XX
CC   This sequence represents a human tumour antigen, NY-ESO-1, the cDNA
CC   encoding which was isolated from an oesophagus squamous cell cancer cDNA
CC   library. Tissue localisation studies revealed it to be expressed at high
CC   levels in normal ovary and testis but not in normal colon, kidney, liver,
CC   brain, oesophagus and skin. It was expressed in certain tumours and
CC   tumour cell lines with some degree of frequency - these included melanoma
CC   specimens and cell lines, and breast and bladder cancer specimens, with
CC   expression in other tumour types being sporadic. Peptides derived from NY
CC   -ESO-1 are bound by both MHC (major histocompatibility complex) Class I
CC   and Class II molecules for presentation to T-cells. Peptides AAY52431-
CC   Y52434 bind to Class I HLA-A2 molecules, thereby stimulating
CC   proliferation of cytotoxic T-cells, while peptides AAY52435-Y52440 bind
CC   to Class II HLA-DR53 molecules, stimulating helper T-cell proliferation.
CC   The peptides derived from NY-ESO-1 may be used in methods and
CC   compositions used for the treatment, diagnosis and prevention of cancers
CC   (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma,
CC   ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to
CC   stimulate the proliferation of T cells
CC
CC   Revised record issued on 21-OCT-2004 : Correction to feature table key
XX
SQ   Sequence 180 AA;
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  Query Match           100.0%;  Score 74;  DB 3;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.052;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 10
AAY70862
ID   AAY70862 standard; protein; 180 AA.
XX
AC   AAY70862;
XX
DT   31-JUL-2000  (first entry)
XX
DE   Human tumour antigen, NY-ESO-1 protein.
XX
KW   NY-ESO-1; CAMEL; CTL-recognised Antigen on MELanoma; human; cancer; CTL;
KW   cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer;
KW   melanoma; immunotherapy; immune response.
XX
OS   Homo sapiens.
XX
PN   WO200023584-A1.
XX
PD   27-APR-2000.
XX
PF   15-OCT-1999;   99WO-EP007832.
XX
PR   16-OCT-1998;   98EP-00119583.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA   (UYHO-) UNIV HOSPITAL LEIDEN.
XX
PI   Schrier PI,  Aarnoudse CA,  Heider K,  Klade C;
XX
DR   WPI; 2000-339685/29.
DR   N-PSDB; AAD00152.
XX
PT   Tumor-associated antigen useful for cancer immunotherapy is encoded by
PT   the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
XX
PS   Example 3; Page 62-63; 73pp; English.
XX
CC   The present sequence is the human NY-ESO-1 protein, a tumour antigen,
CC   identified by screening an esophagus carcinoma cDNA library. This protein
CC   is derived from open reading frame (ORF)-1 that contain epitopes of
CC   tumour specific T-cells. NY-ESO-1 is expressed in different tumour types,
CC   but not in healthy tissues except in testis. It also shows homology with
CC   the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELanoma)
CC   protein, a tumour-asociated antigen. The tumour-associated antigen
CC   displayed on melanoma cells is recognised by cytotoxic T lymphocytes.
CC   This sequence has anticancer activity. CAMEL tumour antigen and
CC   immunogenic peptides derived from it are useful for cancer immunotherapy.
CC   They have the potential to induce an immune response, by eliciting a CTL
CC   response. The DNA molecule is used for the construction of recombinant or
CC   fusion proteins
XX
SQ   Sequence 180 AA;

  Query Match           100.0%;  Score 74;  DB 3;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.052;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 11
```

```
AAB03154
ID   AAB03154 standard; protein; 180 AA.
XX
AC   AAB03154;
XX
DT   23-OCT-2000  (first entry)
XX
DE   Human oesophageal cancer-associated antigen NY-ESO-1.
XX
KW   Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen;
KW   oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain;
KW   antibody; diagnostic marker; drug delivery target.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   7
FT                   /note= "Potential N-myristoylation site"
FT   Modified-site   9
FT                   /note= "Potential N-myristoylation site"
FT   Modified-site   11
FT                   /note= "Potential O-phosphorylation site"
FT   Modified-site   98
FT                   /note= "Potential O-phosphorylation site"
FT   Modified-site   134
FT                   /note= "Potential O-phosphorylation site"
FT   Modified-site   138
FT                   /note= "Potential O-phosphorylation site"
FT   Domain          152. .172
FT                   /note= "Potential transmembrane domain"
XX
PN   US6069233-A.
XX
PD   30-MAY-2000.
XX
PF   26-JAN-1998;   98US-00013150.
XX
PR   03-OCT-1996;   96US-00725381.
XX
PA   (SLOK ) SLOAN KETTERING INST CANCER RES.
PA   (CORR ) CORNELL RES FOUND INC.
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Scanlan M,  Gure AO,  Chen Y,  Tureci O,  Sahin U,  Pfreundschuh M;
PI   Old LJ;
XX
DR   WPI; 2000-410880/35.
DR   N-PSDB; AAA61483.
XX
PT   New isolated esophageal cancer-associated antigen useful as markers for
PT   producing antibodies and as targets for identifying abnormal conditions,
PT   e.g. infections and cancer.
XX
PS   Example 5; Fig 3; 9pp; English.
XX
CC   This sequence represents a human oesophageal cancer-associated antigen,
CC   NY-ESO-1. The cDNA encoding this sequence was isolated from a cDNA
CC   library prepared from a specimen of well-to-moderately differentiated
CC   squamous cell cancer of the oesophagus. Expression analysis demonstrated
CC   that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma
CC   cell lines and in normal ovary and testis tissue, but not in normal
CC   colon, kidney, liver or brain tissue. Analysis of the amino acid sequence
CC   of the protein indicates that the protein has a transmembrane domain,
CC   several N-myristoylation sites and O-phosphorylation sites and that it
CC   contains antigenic sequences in the N-terminal half of the protein. The
CC   antigen is useful as an immunogen when combined with an adjuvant, in both
CC   precursor and post- translationally modified forms, and may be used to
CC   generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic
CC   marker for oesophageal cancer, and can be utilised as a marker for the
CC   targetted delivery of therapeutic agents to oesophageal cancer cells. It
CC   can also be used to generate diagnostic or therapeutic agents
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 74;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.052;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 12
AAB69946
ID   AAB69946 standard; protein; 180 AA.
XX
AC   AAB69946;
XX
DT   27-APR-2001  (first entry)
XX
DE   Human NY-ESO-1 protein.
XX
KW   Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW   HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW   non-small cell lung carcinoma; tumour status determination.
XX
OS   Homo sapiens.
XX
PN   WO200107917-A1.
XX
PD   01-FEB-2001.
XX
PF   14-JUL-2000; 2000WO-US019220.
XX
PR   23-JUL-1999;   99US-00359503.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (SLOK ) SLOAN KETTERING INST CANCER RES.
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Jager E,  Stockert E,  Old LJ,  Knuth A,  Chen Y,  Scanlan M;
XX
DR   WPI; 2001-182822/18.
DR   N-PSDB; AAF58634.
XX
PT   Method useful for determining the status (e.g. progression, regression or
PT   stability of the disease) of a cancerous condition, involves determining
PT   the levels of NY-ESO-1 specific antibodies in a sample taken from a
PT   patient.
XX
PS   Example 5; Fig 3; 50pp; English.
XX
CC   The present sequence is human NY-ESO-1 protein. It is provided in a
CC   specification relating to a method for determining the status of a
CC   cancerous condition in a patient with a tumour that expresses NY-ESO-1.
CC   The method comprises assaying a sample taken from the patient for
CC   antibodies that specifically bind to the NY-ESO-1 and comparing the value
CC   obtained to a prior value obtained from assay of a prior sample taken
CC   from the patient. Any difference between the values is indicative of a
CC   change in status of the cancerous condition. The method is useful for
CC   determining whether a cancerous condition is progressing, regressing or
CC   remaining stable, in particular in patients receiving treatment for a
CC   melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
CC   carcinoma
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 74;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.052;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62
```

```
RESULT 13
AAG67164
ID   AAG67164 standard; protein; 180 AA.
XX
AC   AAG67164;
XX
DT   13-NOV-2001  (first entry)
XX
DE   Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
XX
KW   Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW   HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
KW   cancer; testis tumour.
XX
OS   Homo sapiens.
XX
PN   WO200162917-A1.
XX
PD   30-AUG-2001.
XX
PF   22-JAN-2001; 2001WO-US002126.
XX
PR   22-FEB-2000; 2000US-00510635.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Lethe B,  Boon-Falleur T;
XX
DR   WPI; 2001-550091/61.
DR   N-PSDB; AAH75118.
XX
PT   Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful
PT   for diagnosing testicular tumors.
XX
PS   Example 5; Fig 3; 50pp; English.
XX
CC   The present sequence represents cancer testis tumour antigen NY-ESO-1
CC   (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
CC   least one human leukocyte antigen (HLA) binding peptide, which binds to
CC   Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is
CC   expressed in tumour mRNA and in testis, but not normal colon, kidney,
CC   liver or brain tissue. The presence or level of expression of NY-ESO-1
CC   may be assayed for the diagnosis of cancer, especially testis tumours
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 74;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.052;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 14
AAU01535
ID   AAU01535 standard; protein; 180 AA.
XX
AC   AAU01535;
XX
DT   18-JUL-2001  (first entry)
XX
DE   Human NY-ESO-1 tumour rejection antigen precursor protein.
XX
KW   NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW   major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW   human leukocyte antigen-determining region; disease progression;
KW   disease regression; disease onset; body tissue; body fluid; enzyme label;
KW   radioactive label; monoclonal antibody.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   7
FT                   /note= "Myristoylated"
FT   Modified-site   9
FT                   /note= "Myristoylated"
FT   Modified-site   11
FT                   /note= "Phosphorylated"
FT   Modified-site   98
FT                   /note= "Phosphorylated"
FT   Modified-site   134
FT                   /note= "Phosphorylated"
FT   Modified-site   138
FT                   /note= "Phosphorylated"
XX
PN   WO200123560-A2.
XX
PD   05-APR-2001.
XX
PF   26-SEP-2000; 2000WO-US026411.
XX
PR   29-SEP-1999;   99US-00408036.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Tureci O,  Sahin U,  Pfreundschuh M;
XX
DR   WPI; 2001-266156/27.
DR   N-PSDB; AAS02254.
XX
PT   Polypeptides binding to major histocompatibility complex class II human
PT   leukocyte antigen-determining region molecule having amino acid sequence
PT   found in tumor rejection antigen precursor used for stimulating
PT   proliferation of helper T cells.
XX
PS   Claim 4; Fig 3; 62pp; English.
XX
CC   The sequence represents a human NY-ESO-1 tumour rejection antigen
CC   precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to
CC   major histocompatibility complex (MHC) Class II molecules such as human
CC   leukocyte antigen-determining region (HLA-DR) molecules and stimulate
CC   proliferation of helper T cells. The peptides can be administered to an
CC   HLA-DR positive subject in order to stimulate the helper T cells. An MHC
CC   Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell
CC   or present in free form is useful for this stimulation. The nucleic acid
CC   is useful for screening for a cancerous condition, which involves
CC   contacting a subject sample to a cell line transfected with the
CC   immunoreactive cell (helper T cell), where interaction is indicative of
CC   cancer. In addition, a sample from a patient (for example, a body fluid
CC   or tissue) can be monitored for the amount of the complex present in the
CC   bloodstream. This is useful for determining regression, progression or
CC   onset of a cancerous condition. The method involves contacting the sample
CC   with a radioactive labelled or enzyme labelled monoclonal antibody which
CC   specifically binds with the complex
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 74;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.052;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 15
AAE07714
ID   AAE07714 standard; protein; 180 AA.
XX
AC   AAE07714;
XX
DT   06-NOV-2001  (first entry)
```

XX
DE Human NY ESO-1 protein.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 45. .47
FT /note= "Encoded by CCCGGGGC"
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US002765.
XX
PR 28-JAN-2000; 2000US-0179004P.
PR 29-SEP-2000; 2000US-0237107P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
DR WPI; 2001-496851/54.
DR N-PSDB; AAD14179, AAD14180.
XX
PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis.
XX
PS Example 1; Fig 1; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any given
CC target antigen and/or hapten and to induce tumour-specific humoral-
CC mediated immunity against cancer. The present sequence is human NY ESO-1
CC protein
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62
```

Search completed: March 13, 2006, 19:03:59
Job time : 105.412 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:04:24 ; Search time 16.6353 Seconds
(without alignments)
80.975 Million cell updates/sec

Title: US-09-529-206E-27
Perfect score: 74
Sequence: 1 GAARASGPGGGAPR 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	67.6	82	2	T04476	acclimation protei
2	49	66.2	222	2	T36115	probable oxidoredu
3	48	64.9	351	2	S50754	hypothetical prote
4	48	64.9	1690	2	T35694	ATP dependent DNA
5	45	60.8	173	2	AB3648	flagellar basal-bo
6	44.5	60.1	566	2	T21096	hypothetical prote
7	44.5	60.1	692	2	T21095	hypothetical prote
8	44.5	60.1	730	2	A36226	collagen alpha 1 c
9	44	59.5	220	2	E72464	hypothetical prote
10	44	59.5	269	2	A47008	transcription acti
11	44	59.5	286	2	S04673	H+-transporting tw
12	44	59.5	379	1	A48082	MAP kinase 3 (EC 2
13	44	59.5	900	2	B70694	probable infB - My
14	44	59.5	924	2	F87103	initiation factor
15	44	59.5	1134	2	A41350	adenylate cyclase
16	44	59.5	3190	2	T13828	CREB-binding prote
17	43	58.1	185	2	T36874	hypothetical prote
18	43	58.1	189	2	AE3136	Hypothetical Prote
19	43	58.1	189	2	G98151	hypothetical prote
20	43	58.1	213	2	S42585	DNA-invertase - Rh
21	43	58.1	260	2	T32525	hypothetical prote
22	43	58.1	307	2	B72677	hypothetical prote
23	43	58.1	349	2	S55626	hypothetical prote
24	43	58.1	377	2	S28184	Ca2+/calmodulin-de
25	43	58.1	380	2	JC1451	Ca2+/calmodulin-de
26	43	58.1	571	2	I37405	polypeptide N-acet
27	43	58.1	627	2	T35608	polyketide hydroxy
28	43	58.1	679	2	S02165	regulatory protein
29	43	58.1	954	2	A87431	regulatory protein
30	43	58.1	1028	2	A56038	DNA-binding protei
31	43	58.1	1036	1	A34755	nitrogen regulator
32	43	58.1	1079	2	B70807	hypothetical glyci
33	43	58.1	1213	2	S16356	ovo protein - frui
34	42	56.8	143	2	H87399	peptidyl-tRNA hydr
35	42	56.8	166	2	G75519	conserved hypothet
36	42	56.8	201	2	G72663	hypothetical prote
37	42	56.8	233	2	JC7618	FRAT2 protein - hu
38	42	56.8	266	1	TLBP2X	tail fiber protein
39	42	56.8	327	2	T29031	hypothetical prote
40	42	56.8	333	2	C48423	homeotic protein e
41	42	56.8	335	2	S08341	myristylated alani
42	42	56.8	378	2	C87425	aldose 1-epimerase
43	42	56.8	387	2	T52451	endopeptidase Clp
44	42	56.8	435	2	T15143	hypothetical prote
45	42	56.8	436	2	T36104	conserved hypothet

ALIGNMENTS

RESULT 1
T04476
acclimation protein 2 - barley
C;Species: Hordeum vulgare (barley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04476
R;Phillips, J.R.; Dunn, M.A.; Hughes, M.A.
Plant Mol. Biol. 33, 1013-1023, 1997
A;Title: mRNA stability and localisation of the low temperature responsive barley gene
A;Reference number: Z15367; MUID:97299834; PMID:9154983
A;Accession: T04476
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-82 <PHI>
A;Cross-references: UNIPROT:Q40033; UNIPARC:UPI000009CE5A; EMBL:X97917; NID:g1418969; P
A;Experimental source: cv. Igri
C;Genetics:
A;Gene: blt14.2

Query Match 67.6%; Score 50; DB 2; Length 82;
Best Local Similarity 69.2%; Pred. No. 4.5;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 GAARASGPGGGAP 13
              |||| :| ||| |
Db         31 GAARGAGAGGGVP 43
```

RESULT 2
T36115
probable oxidoreductase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C;Accession: T36115
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1999
A;Reference number: Z21597
A;Accession: T36115
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-222 <MUR>
A;Cross-references: UNIPROT:Q9X887; UNIPARC:UPI00000DB008; EMBL:AL049707; PIDN:CAB41281
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCE15.12c
C;Superfamily: NAD(P)H-dependent FMN reductase (sulfate starvation-induced protein 4);

Query Match 66.2%; Score 49; DB 2; Length 222;
Best Local Similarity 69.2%; Pred. No. 14;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 GAARASGPGGGAP 13
```

```
            |:||||||  | |
Db        181 GSARASGPSAGRP 193
```

RESULT 3
S50754
hypothetical protein WP6 - Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S50754
R;Woessner, J.P.; Molendijk, A.J.; van Egmond, P.; Klis, F.M.; Goodenough, U.W.; Haring,
Plant Mol. Biol. 26, 947-960, 1994
A;Title: Domain conservation in several volvocalean cell wall proteins.
A;Reference number: S50754; MUID:95093034; PMID:8000007
A;Accession: S50754
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-351 <WOE>
A;Cross-references: UNIPROT:Q39492; UNIPARC:UPI00000A170A; EMBL:L29028; NID:g530877; PID

```
  Query Match             64.9%;  Score 48;  DB 2;  Length 351;
  Best Local Similarity   69.2%;  Pred. No. 27;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAP 13
              |: ||| |||| |
Db        296 GSPRASPPGGGPP 308
```

RESULT 4
T35694
ATP dependent DNA helicase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35694
R;Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A;Reference number: Z21587
A;Accession: T35694
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1690 <HAR>
A;Cross-references: UNIPROT:O86821; UNIPARC:UPI00000DACB6; EMBL:AL031031; PIDN:CAA19862.
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC7C7.16c

```
  Query Match             64.9%;  Score 48;  DB 2;  Length 1690;
  Best Local Similarity   64.3%;  Pred. No. 99;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              |:|  ||| | |||
Db       1437 GSANGSGPEGSAPR 1450
```

RESULT 5
AB3648
flagellar basal-body rod protein flgF [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AB3648
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AB3648
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <KUR>
A;Cross-references: UNIPROT:Q8YAZ4; UNIPARC:UPI0000058740; GB:AE008918; PIDN:AAL54349.1;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII1107
A;Map position: II

```
  Query Match             60.8%;  Score 45;  DB 2;  Length 173;
  Best Local Similarity   64.3%;  Pred. No. 37;
  Matches    9;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||     |||||||
Db        125 GAPIVLNPGGGAPR 138
```

RESULT 6
T21096
hypothetical protein F18H3.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21096
R;Coles, L.
submitted to the EMBL Data Library, July 1995
A;Reference number: Z19373
A;Accession: T21096
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-566 <WIL>
A;Cross-references: UNIPROT:Q19581; UNIPARC:UPI0000079311; EMBL:Z50110; PIDN:CAA90446.1
A;Experimental source: clone F18H3
C;Genetics:
A;Gene: CESP:F18H3.3b
A;Map position: X
A;Introns: 111/1; 215/2; 469/3; 552/3
C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology

```
  Query Match             60.1%;  Score 44.5;  DB 2;  Length 566;
  Best Local Similarity   62.5%;  Pred. No. 1.2e+02;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 GAARASGPG---GGAP 13
              || |  |||   ||||
Db        534 GAPRVGGPGVQMGGAP 549
```

RESULT 7
T21095
hypothetical protein F18H3.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21095
R;Coles, L.
submitted to the EMBL Data Library, July 1995
A;Reference number: Z19373
A;Accession: T21095
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-692 <WIL>
A;Cross-references: UNIPROT:Q19579; UNIPARC:UPI0000079A30; EMBL:Z50110; PIDN:CAA90444.1
A;Experimental source: clone F18H3
C;Genetics:
A;Gene: CESP:F18H3.3a
A;Map position: X
A;Introns: 111/1; 215/2; 469/3; 552/3
C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology

```
  Query Match             60.1%;  Score 44.5;  DB 2;  Length 692;
  Best Local Similarity   62.5%;  Pred. No. 1.4e+02;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 GAARASGPG---GGAP 13
              || |  |||   ||||
Db        534 GAPRVGGPGVQMGGAP 549
```

RESULT 8
A36226
collagen alpha 1 chain - sea urchin (Paracentrotus lividus)
C;Species: Paracentrotus lividus (common urchin)
C;Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 09-Jul-2004
C;Accession: A36226
R;D'Alessio, M.; Ramirez, F.; Suzuki, H.R.; Solursh, M.; Gambino, R.
Proc. Natl. Acad. Sci. U.S.A. 86, 9303-9307, 1989
A;Title: Structure and developmental expression of a sea urchin fibrillar collagen gene.
A;Reference number: A36226; MUID:90083256; PMID:2594770
A;Accession: A36226
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-730 <DAA>
A;Cross-references: UNIPROT:Q26052; UNIPARC:UPI000007B305; GB:M25282; NID:g159957; PIDN:
A;Note: the authors translated the codon CAG for residue 136 as Leu, and CAT for residue
C;Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology
C;Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix
F;523-730/Domain: fibrillar collagen carboxyl-terminal homology <FCC>

  Query Match 60.1%; Score 44.5; DB 2; Length 730;
  Best Local Similarity 61.1%; Pred. No. 1.4e+02;
  Matches 11; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

Qy 1 GAARASGPGG-----GAP 13
Db 338 GPAGASGPGGDTGSVGAP 355

RESULT 9
E72464
hypothetical protein APE2360 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: E72464
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: E72464
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-220 <KAW>
A;Cross-references: UNIPROT:Q9Y9C7; UNIPARC:UPI000005E2F9; DDBJ:AP000064; NID:g5105945;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE2360
C;Superfamily: Aeropyrum pernix hypothetical protein APE2360

  Query Match 59.5%; Score 44; DB 2; Length 220;
  Best Local Similarity 57.1%; Pred. No. 62;
  Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAARASGPGGGAPR 14
Db 182 GATRVARPGGGSDR 195

RESULT 10
A47008
transcription activator NF-IL6 beta - human
N;Alternate names: d(CCAAT)-enhancer-binding protein delta, (C/EBP delta); transcription
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47008; A40225
R;Cleutjens, C.B.; van Eekelen, C.C.; van Dekken, H.; Smit, E.M.; Hagemeijer, A.; Wagner
Genomics 16, 520-523, 1993
A;Title: The human C/EBP delta (CRP3/CELF) gene: structure and chromosomal localization.
A;Reference number: A47008; MUID:93300531; PMID:8314590
A;Accession: A47008
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-269 <CLE>
A;Cross-references: UNIPROT:P49716; UNIPARC:UPI00001274A2; GB:S63168; NID:g386449; PIDN
A;Experimental source: prostate carcinoma cell line LNCaP
A;Note: sequence extracted from NCBI backbone (NCBIN:134356, NCBIP:134357)
R;Kinoshita, S.; Akira, S.; Kishimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 89, 1473-1476, 1992
A;Title: A member of the C/EBP family, NF-IL6 beta, forms a heterodimer and transcripti
A;Reference number: A40225; MUID:92159071; PMID:1741402
A;Accession: A40225
A;Molecule type: DNA
A;Residues: 1,'T',3-12,'G',14-269 <KIN>
A;Cross-references: UNIPARC:UPI0000053FFB; GB:M83667; NID:g189175; PIDN:AAA59927.1; PID
A;Note: sequence extracted from NCBI backbone (NCBIN:82662, NCBIP:82663)
C;Genetics:
A;Gene: GDB:CEBPD; CRP3; CELF
A;Cross-references: GDB:132661; OMIM:116898
A;Map position: 8q11-8q11
C;Superfamily: CCAAT/enhancer-binding protein alpha
C;Keywords: leucine zipper; transcription regulation
F;226-254/Region: leucine zipper motif

  Query Match 59.5%; Score 44; DB 2; Length 269;
  Best Local Similarity 64.3%; Pred. No. 73;
  Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAARASGPGGGAPR 14
Db 104 GPARPLGPGPAAPR 117

RESULT 11
S04673
H+-transporting two-sector ATPase (EC 3.6.3.14) gamma chain - Rhodopseudomonas blastica
C;Species: Rhodopseudomonas blastica
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 31-Dec-2004
C;Accession: S04673
R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A;Title: Rhodopseudomonas blastica atp operon. Nucleotide sequence and transcription.
A;Reference number: S04666; MUID:85058188; PMID:6209404
A;Accession: S04673
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-286 <TYB>
A;Cross-references: UNIPROT:P05436; UNIPARC:UPI0000126582
C;Superfamily: H(+)-transporting ATP synthase gamma chain
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

  Query Match 59.5%; Score 44; DB 2; Length 286;
  Best Local Similarity 69.2%; Pred. No. 77;
  Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AARASGPGGGAPR 14
Db 54 ASLASGQGAGAPR 66

RESULT 12
A48082
MAP kinase 3 (EC 2.7.1.-) - human
N;Alternate names: extracellular signal-regulated kinase 1 (ERK1); mitogen-activated pr
N;Contains: protein kinase (EC 2.7.1.37)
C;Species: Homo sapiens (man)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C;Accession: A48082; PQ0270; S23428; S15519; S21579
R;Charest, D.L.; Mordret, G.; Harder, K.W.; Jirik, F.; Pelech, S.L.
Mol. Cell. Biol. 13, 4679-4690, 1993
A;Title: Molecular cloning, expression, and characterization of the human mitogen-activ
A;Reference number: A48082; MUID:93330262; PMID:7687743
A;Accession: A48082
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-379 <CHA>

```
A;Cross-references: UNIPROT:P27361; UNIPARC:UPI0000035BE2; EMBL:X60188; NID:g31220; PIDN
A;Experimental source: hepatoma cell line HEP G2
A;Note: authors translated the codon AGC for residue 174 as Ile
R;Owaki, H.; Makar, R.; Boulton, T.G.; Cobb, M.H.; Geppert, T.D.
Biochem. Biophys. Res. Commun. 182, 1416-1422, 1992
A;Title: Extracellular signal-regulated kinases in T cells: characterization of human ER
A;Reference number: JQ1400; MUID:92171961; PMID:1540184
A;Accession: PQ0270
A;Molecule type: mRNA
A;Residues: 14-173,'I',175-379 <OWA>
A;Cross-references: UNIPARC:UPI000016AB99; GB:M84490; NID:g186695; PIDN:AAA36142.1; PID:
A;Experimental source: cell line CEM
R;Gonzalez, F.A.; Raden, D.L.; Rigby, M.R.; Davis, R.J.
FEBS Lett. 304, 170-178, 1992
A;Title: Heterogeneous expression of four MAP kinase isoforms in human tissues.
A;Reference number: S23426; MUID:92316223; PMID:1319925
A;Accession: S23428
A;Molecule type: mRNA
A;Residues: 25-173,'I',175-379 <GON>
A;Cross-references: UNIPARC:UPI000016A2B4; EMBL:Z11696; NID:g23882; PIDN:CAA77754.1; PID
C;Comment: This enzyme is activated by MAP kinase kinase (see PIR:45100 and PIR:A46723).
C;Genetics:
A;Gene: GDB:PRKM3; ERK1
A;Cross-references: GDB:135679; OMIM:601795
A;Map position: 16pter-16qter
C;Complex: monomer
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Pathway: MAP kinase cascade
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; monomer; phosphoprotein; phosphotransferase; serine/threonine-specific
F;40-330/Domain: protein kinase homology <KIN>
F;48-56/Region: protein kinase ATP-binding motif
F;202/Binding site: phosphate (Thr) (covalent) (by MAP kinase kinase) #status predicted
F;204/Binding site: phosphate (Tyr) (covalent) (by MAP kinase kinase) #status predicted

  Query Match             59.5%;  Score 44;  DB 1;  Length 379;
  Best Local Similarity   69.2%;  Pred. No. 96;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 AARASGPGGGAPR 14
              || | | ||| ||
Db          3 AAAAQGGGGGEPR 15


RESULT 13
B70694
probable infB - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: B70694
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70694
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-900 <COL>
A;Cross-references: UNIPROT:P71613; UNIPARC:UPI000012D2E2; GB:Z81331; GB:AL123456; NID:g
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: infB
C;Superfamily: translation initiation factor IF-2; translation elongation factor Tu homo
C;Keywords: GTP binding; nucleotide binding; P-loop
F;399-512/Domain: translation elongation factor Tu homology <ETU>
F;405-412/Region: nucleotide-binding motif A (P-loop)
F;509-512/Region: GTP-binding NKXD motif
F;545-547/Region: GTP-binding SAK/L motif
F;411,412,432,509,510,512,545/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #

  Query Match             59.5%;  Score 44;  DB 2;  Length 900;
  Best Local Similarity   71.4%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||| | |  |||||
Db        262 GAAGAFGRPGGAPR 275


RESULT 14
F87103
initiation factor IF-2 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F87103
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: F87103
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-924 <STO>
A;Cross-references: UNIPROT:Q9Z5I9; UNIPARC:UPI000012D2E0; GB:AL450380; NID:g13093370;
C;Genetics:
A;Gene: infB
C;Superfamily: translation initiation factor IF-2; translation elongation factor Tu hom

  Query Match             59.5%;  Score 44;  DB 2;  Length 924;
  Best Local Similarity   71.4%;  Pred. No. 2e+02;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||| | |  |||||
Db        286 GAAGAFGRPGGAPR 299


RESULT 15
A41350
adenylate cyclase (EC 4.6.1.1), brain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C;Accession: A41350
R;Krupinski, J.; Coussen, F.; Bakalyar, H.A.; Tang, W.J.; Feinstein, P.G.; Orth, K.; Sla
Science 244, 1558-1564, 1989
A;Title: Adenylyl cyclase amino acid sequence: possible channel- or transporter-like str
A;Reference number: A41350; MUID:89298382; PMID:2472670
A;Accession: A41350
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1134 <KRU>
A;Cross-references: UNIPROT:P19754; UNIPARC:UPI000012886C; GB:M25579; NID:g162612; PIDN
C;Superfamily: human adenylate cyclase; guanylate cyclase catalytic domain homology
C;Keywords: phosphorus-oxygen lyase; transmembrane protein
F;248-482/Domain: guanylate cyclase catalytic domain homology <GCC>
F;819-1061/Domain: guanylate cyclase catalytic domain homology <GCC2>

  Query Match             59.5%;  Score 44;  DB 2;  Length 1134;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+02;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGG 10
              || ||:||||
Db         22 GAERAAGPGG 31


Search completed: March 13, 2006, 19:16:10
Job time : 16.6353 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 18:53:23 ; Search time 101.624 Seconds
(without alignments)
97.196 Million cell updates/sec

Title: US-09-529-206E-27
Perfect score: 74
Sequence: 1 GAARASGPGGGAPR 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	74	100.0	142	2	Q9NY13_HUMAN	Q9ny13 homo sapien
2	74	100.0	180	1	CTG1B_HUMAN	P78358 homo sapien
3	74	100.0	180	2	Q7LBY4_HUMAN	Q7lby4 homo sapien
4	66	89.2	210	1	CTAG2_HUMAN	O75638 homo sapien
5	54	73.0	362	2	Q63QT8_BURPS	Q63qt8 burkholderi
6	54	73.0	362	2	Q62H22_BURMA	Q62h22 burkholderi
7	52	70.3	321	2	Q96S27_HUMAN	Q96s27 homo sapien
8	52	70.3	447	2	Q9GRA8_GRYBI	Q9gra8 gryllus bim
9	52	70.3	644	2	Q688J5_ORYSA	Q688j5 oryza sativ
10	51	68.9	337	1	CT086_HUMAN	Q9bz19 homo sapien
11	51	68.9	367	2	Q6AV33_ORYSA	Q6av33 oryza sativ
12	51	68.9	559	2	Q8L680_ORYSA	Q8l680 oryza sativ
13	51	68.9	867	2	Q94LD1_ORYSA	Q94ld1 oryza sativ
14	50	67.6	82	2	Q40033_HORVU	Q40033 hordeum vul
15	50	67.6	111	2	Q5NTA5_CANFA	Q5nta5 canis famil
16	50	67.6	194	2	Q96BU2_HUMAN	Q96bu2 homo sapien
17	50	67.6	895	2	Q4NUK4_9DELT	Q4nuk4 anaeromyxob
18	50	67.6	896	2	Q96D18_HUMAN	Q96d18 homo sapien
19	50	67.6	1253	2	Q6DHV6_HUMAN	Q6dhv6 homo sapien
20	50	67.6	1430	2	Q9H7P9_HUMAN	Q9h7p9 homo sapien
21	49	66.2	175	1	PACA_CHICK	P41534 g glucagon-
22	49	66.2	222	2	Q9X887_STRCO	Q9x887 streptomyce
23	49	66.2	322	2	Q67PJ0_SYMTH	Q67pj0 symbiobacte
24	49	66.2	327	2	Q63HT9_BURPS	Q63ht9 burkholderi
25	49	66.2	330	2	Q629N3_BURMA	Q629n3 burkholderi
26	49	66.2	457	2	Q7G604_ORYSA	Q7g604 oryza sativ
27	49	66.2	457	2	Q94LK1_ORYSA	Q941k1 oryza sativ
28	49	66.2	564	2	Q4NNS9_9DELT	Q4nns9 anaeromyxob
29	49	66.2	589	2	Q8H3F8_ORYSA	Q8h3f8 oryza sativ
30	49	66.2	695	2	Q4T320_TETNG	Q4t320 tetraodon n
31	49	66.2	713	2	Q4NW70_9DELT	Q4nw70 anaeromyxob
32	49	66.2	788	2	Q4QQP8_HUMAN	Q4qqp8 homo sapien
33	49	66.2	1379	2	Q7QEK5_ANOGA	Q7qek5 anopheles g
34	48.5	65.5	924	2	Q4NQS2_9DELT	Q4nqs2 anaeromyxob
35	48	64.9	88	2	Q4RDF1_TETNG	Q4rdf1 tetraodon n
36	48	64.9	159	2	Q63KC9_BURPS	Q63kc9 burkholderi
37	48	64.9	159	2	Q62DA7_BURMA	Q62da7 burkholderi
38	48	64.9	207	2	Q8H5I9_ORYSA	Q8h5i9 oryza sativ
39	48	64.9	262	2	Q5Z8E2_ORYSA	Q5z8e2 oryza sativ
40	48	64.9	351	2	Q39492_CHLEU	Q39492 chlamydomon
41	48	64.9	449	2	Q7F1E3_ORYSA	Q7f1e3 oryza sativ
42	48	64.9	487	2	Q5RL80_HUMAN	Q5rl80 homo sapien
43	48	64.9	542	2	Q4UVF6_XANCP	Q4uvf6 xanthomonas
44	48	64.9	558	2	Q4NUC4_9DELT	Q4nuc4 anaeromyxob
45	48	64.9	717	2	Q51TX7_MAGGR	Q51tx7 magnaporthe

ALIGNMENTS

```
RESULT 1
Q9NY13_HUMAN
ID   Q9NY13_HUMAN PRELIMINARY;      PRT;   142 AA.
AC   Q9NY13;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical protein LAGE-2 (Fragment).
GN   Name=LAGE-2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lethe B.G.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ275978; CAB76945.1; -; mRNA.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   142 AA;  13895 MW;  27EBE922AC4ACC7B CRC64;

  Query Match             100.0%;  Score 74;  DB 2;  Length 142;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         23 GAARASGPGGGAPR 36


RESULT 2
CTG1B_HUMAN
ID   CTG1B_HUMAN    STANDARD;      PRT;   180 AA.
AC   P78358;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-
DE   ESO-1).
GN   Name=CTAG1B; Synonyms=CTAG, CTAG1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
RA   Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,
RA   Williamson B., Stockert E., Pfreundschuh M., Old L.J.;
RT   "A testicular antigen aberrantly expressed in human cancers detected
RT   by autologous antibody screening.";
```

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RL   Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Melanoma;
RX   MEDLINE=98289662; PubMed=9626360;
RA   Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA   de Plaen E., Boon T.;
RT   "LAGE-1, a new gene with tumor specificity.";
RL   Int. J. Cancer 76:903-908(1998).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98430682; PubMed=9759882;
RA   Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,
RA   Schwartzentruber D.J., Rosenberg S.A.;
RT   "A breast and melanoma-shared tumor antigen: T cell responses to
RT   antigenic peptides translated from different open reading frames.";
RL   J. Immunol. 161:3596-3606(1998).
CC   -!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide
CC       variety of cancers. Detected in uterine myometrium.
CC   -!- SIMILARITY: Belongs to the CTAG family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U87459; AAB49693.1; -; mRNA.
DR   EMBL; AJ003149; CAA05908.1; -; mRNA.
DR   EMBL; AF038567; AAD05202.1; -; mRNA.
DR   HGNC; HGNC:2491; CTAG1B.
DR   MIM; 300156; -.
KW   Antigen; Transmembrane.
FT   TRANSMEM    156    172       Potential.
FT   COMPBIAS      5     82       Gly-rich.
SQ   SEQUENCE   180 AA;  17992 MW;  B122C5C2C8BE1569 CRC64;

  Query Match             100.0%;  Score 74;  DB 1;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.031;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 3
Q7LBY4_HUMAN
ID   Q7LBY4_HUMAN PRELIMINARY;      PRT;   180 AA.
AC   Q7LBY4;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
DE   antigen 1-A).
GN   Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21303268;
RA   Galgoczy P., Rosenthal A., Platzer M.;
RT   "Human-mouse comparative sequence analysis of the NEMO gene reveals an
RT   alternative promoter within the neighboring G6PD gene.";
RL   Gene 271:93-98(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21566154; PubMed=11709543; DOI=10.1093/hmg/10.22.2557;
RA   Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
RA   Patlan H., Ciccodicola A., Kenwrick S., Platzer M., D'Urso M.,
RA   Nelson D.L.;
RT   "Multiple pathogenic and benign genomic rearrangements occur at a 35
RT   kb duplication involving the NEMO and LAGE2 genes.";
RL   Hum. Mol. Genet. 10:2557-2567(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Platzer M.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Platzer M.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RA   Galgoczy P., Platzer M.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99454989; PubMed=10523621;
RA   De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
RT   "DNA methylation is the primary silencing mechanism for a set of germ
RT   line- and tumor-specific genes with a CpG-rich promoter.";
RL   Mol. Cell. Biol. 19:7327-7335(1999).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RA   Lethe B.G.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF277315; AAL27014.1; -; Genomic_DNA.
DR   EMBL; AJ275977; CAB76943.1; -; Genomic_DNA.
DR   EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
SQ   SEQUENCE   180 AA;  17992 MW;  B122C5C2C8BE1569 CRC64;

  Query Match             100.0%;  Score 74;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.031;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 4
CTAG2_HUMAN
ID   CTAG2_HUMAN    STANDARD;      PRT;   210 AA.
AC   O75638; O75637; Q9BU80; Q9UJ89; Q9Y479;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
GN   Name=CTAG2; Synonyms=ESO2, LAGE1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B).
RC   TISSUE=Melanoma;
RX   MEDLINE=98289662; PubMed=9626360;
RA   Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA   de Plaen E., Boon T.;
RT   "LAGE-1, a new gene with tumor specificity.";
RL   Int. J. Cancer 76:903-908(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B), AND VARIANTS
RP   GLN-6; GLN-89 AND ARG-138.
RC   TISSUE=Melanoma;
RX   MEDLINE=99325550; PubMed=10399963;
RA   Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT   "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT   unexpected translation product of LAGE-1.";
RL   Int. J. Cancer 82:442-448(1999).
RN   [3]
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RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
RP   ARG-138.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=LAGE-1B; Synonyms=LAGE-1L;
CC         IsoId=O75638-1; Sequence=Displayed;
CC       Name=LAGE-1A; Synonyms=LAGE-1S;
CC         IsoId=O75638-2; Sequence=VSP_004301;
CC   -!- TISSUE SPECIFICITY: Testis and very low level in placenta and in
CC       some uterus samples. Observed in 25-50% of tumor samples of
CC       melanomas, non-small-cell lung carcinomas, bladder, prostate and
CC       head and neck cancers.
CC   -!- DOMAIN: A transmembrane domain is present in isoform LAGE-1A.
CC   -!- SIMILARITY: Belongs to the CTAG family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AJ223093; CAA11117.1; -; Genomic_DNA.
DR   EMBL; AJ223093; CAA11116.1; -; Genomic_DNA.
DR   EMBL; AJ223040; CAA11043.1; -; mRNA.
DR   EMBL; AJ223041; CAA11044.1; -; mRNA.
DR   EMBL; AJ012834; CAA10194.1; -; mRNA.
DR   EMBL; AJ012835; CAA10196.1; -; mRNA.
DR   EMBL; BC002833; AAH02833.1; -; mRNA.
DR   Ensembl; ENSG00000126890; Homo sapiens.
DR   HGNC; HGNC:2492; CTAG2.
DR   H-InvDB; HIX0017163; -.
DR   MIM; 300396; -.
KW   Alternative splicing; Antigen; Polymorphism; Transmembrane.
FT   COMPBIAS      5     79       Gly-rich.
FT   COMPBIAS    183    188       Poly-Pro.
FT   VARSPLIC    135    210       MSVWDQDREGAGRMRVVGWGLGSASPEGQKARDLRTPKHKV
FT                                SEQRPGTPGPPPPEGAQGDGCRGVAFNVMFSAPHI -> IR
FT                                LTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQAPSG
FT                                QRR (in isoform LAGE-1A).
FT                                /FTId=VSP_004301.
FT   VARIANT       6      6       R -> Q.
FT                                /FTId=VAR_007855.
FT   VARIANT      89     89       E -> Q.
FT                                /FTId=VAR_007856.
FT   VARIANT     138    138       W -> R.
FT                                /FTId=VAR_007857.
SQ   SEQUENCE   210 AA;  21120 MW;  8BE0EE00AE55E8BE CRC64;

  Query Match             89.2%;  Score 66;  DB 1;  Length 210;
  Best Local Similarity   92.9%;  Pred. No. 0.42;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||| |||||
Db         49 GAARASGPRGGAPR 62


RESULT 5
Q63QT8_BURPS
ID   Q63QT8_BURPS PRELIMINARY;      PRT;   362 AA.
AC   Q63QT8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative DNA polymerase III.
GN   OrderedLocusNames=BPSL2936;
OS   Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia; pseudomallei group.
OX   NCBI_TaxID=28450;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=K96243;
RX   PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA   Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
RA   Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA   Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
RA   Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA   Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D.,
RA   Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA   Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA   Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA   Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA   Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT   "Genomic plasticity of the causative agent of melioidosis,
RT   Burkholderia pseudomallei.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR   EMBL; BX571965; CAH36946.1; -; Genomic_DNA.
DR   GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR   GO; GO:0006260; P:DNA replication; IEA.
DR   InterPro; IPR010372; DNA_pol3_delta.
DR   InterPro; IPR005790; DNA_polIII_delta.
DR   Pfam; PF06144; DNA_pol3_delta; 1.
DR   TIGRFAMs; TIGR01128; holA; 1.
KW   Complete proteome.
SQ   SEQUENCE   362 AA;  38726 MW;  D5FF3DE783D41E41 CRC64;

  Query Match             73.0%;  Score 54;  DB 2;  Length 362;
  Best Local Similarity   83.3%;  Pred. No. 28;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 ARASGPGGGAPR 14
              |||:|||| |||
Db        348 ARAAGPGGDAPR 359


RESULT 6
Q62H22_BURMA
ID   Q62H22_BURMA PRELIMINARY;      PRT;   362 AA.
AC   Q62H22;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   DNA polymerase III, delta subunit (EC 2.7.7.7).
GN   Name=holA; OrderedLocusNames=BMA2451;
OS   Burkholderia mallei (Pseudomonas mallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia.
OX   NCBI_TaxID=13373;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ATCC 23344;
RX   PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA   Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
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RA   Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA   Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA   Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA   Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
RA   Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA   Zafar N., Zhou L., Fraser C.M.;
RT   "Structural flexibility in the Burkholderia mallei genome.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR   EMBL; CP000010; AAU49707.1; -; Genomic_DNA.
DR   TIGR; BMA2451; -.
DR   GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006260; P:DNA replication; IEA.
DR   InterPro; IPR010372; DNA_pol3_delta.
DR   InterPro; IPR005790; DNA_polIII_delta.
DR   Pfam; PF06144; DNA_pol3_delta; 1.
DR   TIGRFAMs; TIGR01128; holA; 1.
KW   Complete proteome; Nucleotidyltransferase; Transferase.
SQ   SEQUENCE   362 AA;  38726 MW;  D5FF3DE783D41E41 CRC64;

  Query Match             73.0%;  Score 54;  DB 2;  Length 362;
  Best Local Similarity   83.3%;  Pred. No. 28;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 ARASGPGGGAPR 14
              |||:|||| |||
Db        348 ARAAGPGGDAPR 359


RESULT 7
Q96S27_HUMAN
ID   Q96S27_HUMAN PRELIMINARY;      PRT;   321 AA.
AC   Q96S27;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein gene X.
GN   Name=gene X;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21096910; PubMed=11157797; DOI=10.1093/hmg/10.4.339;
RA   Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA   Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA   Higgs D.R.;
RT   "Sequence, structure and pathology of the fully annotated terminal 2
RT   Mb of the short arm of human chromosome 16.";
RL   Hum. Mol. Genet. 10:339-352(2001).
DR   EMBL; AE006463; AAK61225.1; -; Genomic_DNA.
DR   Ensembl; ENSG00000167933; Homo sapiens.
KW   Hypothetical protein.
SQ   SEQUENCE   321 AA;  32979 MW;  9C8764CFA17F4CD4 CRC64;

  Query Match             70.3%;  Score 52;  DB 2;  Length 321;
  Best Local Similarity   76.9%;  Pred. No. 46;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AARASGPGGGAPR 14
              ||| :|||||| |
Db          5 AARRAGPGGGAAR 17


RESULT 8
Q9GRA8_GRYBI
ID   Q9GRA8_GRYBI PRELIMINARY;      PRT;   447 AA.
AC   Q9GRA8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hedgehog protein (Fragment).
OS   Gryllus bimaculatus (Two-spotted cricket).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC   Gryllus.
OX   NCBI_TaxID=6999;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20461145; PubMed=11003837;
RA   Niwa N., Inoue Y., Nozawa A., Saito M., Misumi Y., Ohuchi H.,
RA   Yoshioka H., Noji S.;
RT   "Correlation of diversity of leg morphology in Gryllus bimaculatus
RT   (cricket) with divergence in dpp expression pattern during leg
RT   development.";
RL   Development 127:4373-4381(2000).
DR   EMBL; AB044709; BAB19658.1; -; mRNA.
DR   HSSP; Q62226; 1VHH.
DR   SMR; Q9GRA8; 49-205.
DR   MEROPS; C46.001; -.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0007267; P:cell-cell signaling; IEA.
DR   GO; GO:0007275; P:development; IEA.
DR   GO; GO:0016539; P:intein-mediated protein splicing; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR003586; Hedgehog_hint_C.
DR   InterPro; IPR003587; Hedgehog_hint_N.
DR   InterPro; IPR000320; HH_signal.
DR   InterPro; IPR006141; Intein_S.
DR   InterPro; IPR001657; Peptidase_C46.
DR   InterPro; IPR001767; Pept_C46_hint.
DR   Pfam; PF01085; HH_signal; 1.
DR   Pfam; PF01079; Hint; 1.
DR   PRINTS; PR00632; SONICHHOG.
DR   SMART; SM00305; HintC; 1.
DR   SMART; SM00306; HintN; 1.
DR   PROSITE; PS50817; INTEIN_N_TER; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   447 AA;  48008 MW;  29AEFB061C3EE6F0 CRC64;

  Query Match             70.3%;  Score 52;  DB 2;  Length 447;
  Best Local Similarity   78.6%;  Pred. No. 63;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||| ||| || |
Db         30 GAARACGPGRGAGR 43


RESULT 9
Q688J5_ORYSA
ID   Q688J5_ORYSA PRELIMINARY;      PRT;   644 AA.
AC   Q688J5;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein OSJNBb0012G21.2.
GN   Name=OSJNBb0012G21.2;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA   Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA   Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA   Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA   Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA   Wu H.-P., Shaw J.-F.;
RT   "Oryza sativa BAC OSJNBb0012G21 genomic sequence.";
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC135421; AAU10755.1; -; Genomic_DNA.
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DR   Gramene; Q688J5; -.
DR   GO; GO:0004057; F:arginyltransferase activity; IEA.
DR   GO; GO:0016598; P:protein arginylation; IEA.
DR   GO; GO:0042176; P:regulation of protein catabolism; IEA.
DR   InterPro; IPR007472; ATE_C.
DR   InterPro; IPR007471; ATE_N.
DR   Pfam; PF04377; ATE_C; 1.
DR   Pfam; PF04376; ATE_N; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   644 AA;  72444 MW;  DDB97FC0C40C23F8 CRC64;

  Query Match           70.3%;  Score 52;  DB 2;  Length 644;
  Best Local Similarity  90.9%;  Pred. No. 88;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGG 11
              ||| |||||||
Db          9 GAASASGPGGG 19


RESULT 10
CT086_HUMAN
ID   CT086_HUMAN    STANDARD;      PRT;   337 AA.
AC   Q9BZ19;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Hypothetical protein C20orf86.
GN   Name=C20orf86;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA   Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA   Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA   Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA   Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA   Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA   Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA   Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA   Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA   Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA   Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA   Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA   Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
CC   -!- SIMILARITY: Contains 2 ANK repeats.
CC   -!- SIMILARITY: Contains 1 ubiquitin-like domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AL354776; CAC17565.2; -; Genomic_DNA.
DR   HSSP; P42771; 2A5E.
DR   Ensembl; ENSG00000124227; Homo sapiens.
DR   HGNC; HGNC:16217; C20orf86.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR000626; Ubiquitin.
DR   Pfam; PF00023; Ank; 2.
DR   PRINTS; PR01415; ANKYRIN.
DR   SMART; SM00248; ANK; 2.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 2.
DR   PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
DR   PROSITE; PS50053; UBIQUITIN_2; 1.
KW   ANK repeat; Hypothetical protein; Polymorphism; Repeat.
FT   DOMAIN       88    164       Ubiquitin-like.
FT   REPEAT      211    241       ANK 1.
FT   REPEAT      244    273       ANK 2.
FT   VARIANT     287    287       R -> C (in dbSNP:584855).
FT                                /FTId=VAR_014400.
SQ   SEQUENCE   337 AA;  36714 MW;  EC8BA4AD414756CB CRC64;

  Query Match           68.9%;  Score 51;  DB 1;  Length 337;
  Best Local Similarity  71.4%;  Pred. No. 66;
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Qy          1 GAARASGPGGGAPR 14
              | |||:|| ||| |
Db          9 GGARAAGPTGGASR 22


RESULT 11
Q6AV33_ORYSA
ID   Q6AV33_ORYSA PRELIMINARY;      PRT;   367 AA.
AC   Q6AV33;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein OSJNBa0063J18.9.
GN   Name=OSJNBa0063J18.9;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA   Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA   Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA   Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA   Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA   White O., Salzberg S.L., Fraser C.M.;
RT   "Oryza sativa chromosome 3 BAC OSJNBa0063J18 genomic sequence.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell R.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC107206; AAT77052.1; -; Genomic_DNA.
DR   Gramene; Q6AV33; -.
KW   Hypothetical protein.
SQ   SEQUENCE   367 AA;  37474 MW;  B8C62D9D4CC18C86 CRC64;

  Query Match           68.9%;  Score 51;  DB 2;  Length 367;
  Best Local Similarity  76.9%;  Pred. No. 71;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 AARASGPGGGAPR 14
              || |||||||: |
Db         91 AAAASGPGGGSAR 103


RESULT 12
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Q8L680_ORYSA
ID   Q8L680_ORYSA PRELIMINARY;      PRT;   559 AA.
AC   Q8L680;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Hypothetical protein OSJNBa0011L09.12.
GN   ORFNames=OSJNBa0011L09.12;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA   Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
RA   Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
RA   Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA   Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell R.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   The Rice Chromosome 10 Sequencing Consortium;
RT   "In-depth view of structure, activity, and evolution of rice
RT   chromosome 10.";
RL   Science 300:1566-1569(2003).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC092388; AAM22719.1; -; Genomic_DNA.
DR   EMBL; AE017090; AAP53592.1; -; Genomic_DNA.
DR   Gramene; Q8L680; -.
DR   InterPro; IPR007228; DUF390.
DR   InterPro; IPR007321; Transposase_28.
DR   Pfam; PF04094; DUF390; 2.
DR   Pfam; PF04195; Transposase_28; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   559 AA;  58950 MW;  A5B4492C2D3F94FA CRC64;

  Query Match             68.9%;  Score 51;  DB 2;  Length 559;
  Best Local Similarity   64.3%;  Pred. No. 1e+02;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              | :| ||||||  |
Db        277 GGSRTSGPGGGGSR 290


RESULT 13
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ID   Q94LD1_ORYSA PRELIMINARY;      PRT;   867 AA.
AC   Q94LD1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein OSJNBa0026A15.11.
GN   Name=OSJNBa0026A15.11;
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
RA   Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
RA   Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.E.,
RA   Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
RA   White O., Fraser C.M.;
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC084404; AAK50601.1; -; Genomic_DNA.
DR   Gramene; Q94LD1; -.
DR   InterPro; IPR007228; DUF390.
DR   InterPro; IPR007321; Transposase_28.
DR   Pfam; PF04094; DUF390; 3.
DR   Pfam; PF04195; Transposase_28; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   867 AA;  92812 MW;  7365009715EDDC21 CRC64;

  Query Match             68.9%;  Score 51;  DB 2;  Length 867;
  Best Local Similarity   64.3%;  Pred. No. 1.6e+02;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              | :|| |||||  |
Db        206 GGSRAGGPGGGGSR 219


RESULT 14
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ID   Q40033_HORVU PRELIMINARY;      PRT;    82 AA.
AC   Q40033;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   BLT14.2 protein.
GN   Name=blt14.2;
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=97299834; PubMed=9154983; DOI=10.1023/A:1005717613224;
RA   Phillips J.R., Dunn M.A., Hughes M.A.;
RT   "mRNA stability and localisation of the low temperature responsive
RT   barley gene family blt14.";
RL   Plant Mol. Biol. 33:1013-1023(1997).
DR   EMBL; X97917; CAA66490.1; -; Genomic_DNA.
DR   PIR; T04476; T04476.
SQ   SEQUENCE   82 AA;  7752 MW;  FA952DCA3CD640A7 CRC64;

  Query Match             67.6%;  Score 50;  DB 2;  Length 82;
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  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAP 13
              |||| :| ||| |
Db         31 GAARGAGAGGGVP 43


RESULT 15
Q5NTA5_CANFA
ID   Q5NTA5_CANFA PRELIMINARY;      PRT;   111 AA.
AC   Q5NTA5;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Pancreatic duodenal homeobox gene 1 (Fragment).
GN   Name=PDX-1;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
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RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Takagi K., Neo S., Furuichi M., Watanabe M., Kansaku N., Hisasue M.,
RA   Tsuchiya R., Yamada T.;
RT   "Canine Pdx-1.";
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB196439; BAD77930.1; -; mRNA.
DR   GO; GO:0005634; C:nucleus; IEA.
KW   Nuclear protein.
FT   NON_TER       1      1
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11740 MW;  4565A9E88EDEC91E CRC64;

  Query Match             67.6%;  Score 50;  DB 2;  Length 111;
  Best Local Similarity   64.3%;  Pred. No. 32;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              | :||| |||  ||
Db         15 GGSRASSPGGAQPR 28


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Job time : 102.624 secs
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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:14:49 ; Search time 26.0235 Seconds
(without alignments)
44.477 Million cell updates/sec

Title: US-09-529-206E-27
Perfect score: 74
Sequence: 1 GAARASGPGGGAPR 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	74	100.0	180	1	US-08-791-495-9	Sequence 9, Appli
2	74	100.0	180	2	US-08-937-263B-8	Sequence 8, Appli
3	74	100.0	180	2	US-09-751-798-8	Sequence 8, Appli
4	74	100.0	180	2	US-09-392-714-25	Sequence 25, Appl
5	74	100.0	180	2	US-09-165-546D-15	Sequence 15, Appl
6	74	100.0	180	2	US-09-341-829A-9	Sequence 9, Appli
7	74	100.0	180	2	US-09-849-602-30	Sequence 30, Appl
8	66	89.2	180	1	US-08-791-495-7	Sequence 7, Appli
9	66	89.2	180	2	US-09-341-829A-7	Sequence 7, Appli
10	66	89.2	210	1	US-08-791-495-5	Sequence 5, Appli
11	66	89.2	210	2	US-09-341-829A-5	Sequence 5, Appli
12	54	73.0	456	2	US-09-252-991A-17335	Sequence 17335, A
13	52	70.3	210	2	US-09-252-991A-24923	Sequence 24923, A
14	50	67.6	160	2	US-09-252-991A-17249	Sequence 17249, A
15	49	66.2	143	2	US-08-789-329C-10	Sequence 10, Appl
16	49	66.2	172	2	US-08-789-329C-7	Sequence 7, Appli
17	49	66.2	175	2	US-08-789-329C-3	Sequence 3, Appli
18	49	66.2	416	2	US-09-252-991A-30219	Sequence 30219, A
19	48	64.9	9	2	US-09-344-040C-117	Sequence 117, App
20	48	64.9	9	2	US-09-833-039A-117	Sequence 117, App
21	48	64.9	196	2	US-09-252-991A-30527	Sequence 30527, A
22	48	64.9	329	2	US-09-252-991A-19752	Sequence 19752, A
23	48	64.9	421	2	US-09-252-991A-32326	Sequence 32326, A
24	48	64.9	809	2	US-09-252-991A-31759	Sequence 31759, A
25	48	64.9	1427	2	US-09-252-991A-20577	Sequence 20577, A
26	47.5	64.2	268	2	US-09-252-991A-31279	Sequence 31279, A
27	47	63.5	370	2	US-09-252-991A-23998	Sequence 23998, A
28	46.5	62.8	678	2	US-10-104-047-3295	Sequence 3295, Ap
29	46	62.2	366	2	US-09-902-540-13196	Sequence 13196, A
30	46	62.2	789	2	US-09-252-991A-25611	Sequence 25611, A
31	45.5	61.5	836	2	US-09-491-356C-21	Sequence 21, Appl
32	45	60.8	134	2	US-09-252-991A-26710	Sequence 26710, A
33	45	60.8	187	2	US-09-252-991A-29442	Sequence 29442, A
34	45	60.8	191	2	US-09-252-991A-23951	Sequence 23951, A
35	45	60.8	262	2	US-09-252-991A-19030	Sequence 19030, A
36	45	60.8	321	1	US-08-362-670B-26	Sequence 26, Appl
37	45	60.8	321	2	US-08-333-576C-26	Sequence 26, Appl
38	45	60.8	321	2	US-08-808-324-26	Sequence 26, Appl
39	45	60.8	321	2	US-09-945-182-26	Sequence 26, Appl
40	45	60.8	321	4	PCT-US94-14030A-26	Sequence 26, Appl
41	45	60.8	679	2	US-09-252-991A-27111	Sequence 27111, A
42	45	60.8	727	2	US-09-902-540-12383	Sequence 12383, A
43	45	60.8	950	2	US-09-252-991A-25927	Sequence 25927, A
44	44	59.5	186	2	US-09-252-991A-16943	Sequence 16943, A
45	44	59.5	242	2	US-08-220-602B-23	Sequence 23, Appl

ALIGNMENTS

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RESULT 1
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL-1 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-791-495-9

  Query Match             100.0%;  Score 74;  DB 1;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
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Db         49 GAARASGPGGGAPR 62
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RESULT 2
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
;  GENERAL INFORMATION:
;    APPLICANT:  Chen, Yao-Tseng; Scanlan, Matthew;
;    APPLICANT:  Gure, Ali; Old, Lloyd J.; Jager, Elke;
;    APPLICANT:  Alexander, Knuth; Drijfhout, Jan W.
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULE
;    TITLE OF INVENTION:  ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
;    TITLE OF INVENTION:  ITSELF, AND USES THEREOF
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/937,263B
;      FILING DATE:  September 15, 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sinn, Eric, Patent Agent
;      REGISTRATION NUMBER:  40,177
;      REFERENCE/DOCKET NUMBER:  LUD 5466.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3000
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-937-263B-8

  Query Match             100.0%;  Score 74;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
;  GENERAL INFORMATION:
;    APPLICANT:  Stockert, Elisabeth; Jager, Elke;
;    APPLICANT:  Chen, Yao-tseng; Scanlan, Matthew;
;    APPLICANT:  Knuth, Alexander; Old, Lloyd J.
;    TITLE OF INVENTION:  Antibodies Which Bind to NY-ESO-1 Cancer
;    TITLE OF INVENTION:  Associated Proteins, Uses Thereof,
;    TITLE OF INVENTION:  Truncated Forms of NY-ESO-1, and HLA
;    TITLE OF INVENTION:  Binding Peptides Derived Therefrom
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/751,798
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/062,422
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 6525177man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3168
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-09-751-798-8

  Query Match             100.0%;  Score 74;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 4
US-09-392-714-25
; Sequence 25, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT: Gure, Ali O.
;  APPLICANT: Williamson, Barbara
;  APPLICANT: Chen, Yao-Tseng
;  APPLICANT: Old, Lloyd J.
;  TITLE OF INVENTION: Cancer Associated Antigens and Uses
;  TITLE OF INVENTION: Therefor
;  FILE REFERENCE: L0461/7062
;  CURRENT APPLICATION NUMBER: US/09/392,714A
;  CURRENT FILING DATE: 1999-09-09
;  EARLIER APPLICATION NUMBER: PCT/US98/14679
;  EARLIER FILING DATE: 1998-07-15
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-392-714-25

  Query Match             100.0%;  Score 74;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
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Db         49 GAARASGPGGGAPR 62
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RESULT 5
US-09-165-546D-15
; Sequence 15, Application US/09165546D
; Patent No. 6723832
;   GENERAL INFORMATION:
;        APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
;                   Gure, Ali, Old, Lloyd, Ritter, Gerd
;        TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                            SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
;                            USES THEREOF
;        NUMBER OF SEQUENCES: 15
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FULBRIGHT & JAWORSKI LLP
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10158
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/165,546D
;             FILING DATE: 02-Oct-1998
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: April 17, 1998
;             APPLICATION NUMBER: 08/937,263
;             FILING DATE: September 15, 1997
;             APPLICATION NUMBER: US 08/725,182
;             FILING DATE: October 3, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, No. 6723832man D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3000
;             TELEFAX: (212) 318-3400
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 180 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15

  Query Match             100.0%;  Score 74;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 6
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-9

  Query Match             100.0%;  Score 74;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 7
US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT:  Old, Lloyd J.
;  APPLICANT:  Stockert, Elisabeth
;  APPLICANT:  Chen, Yao-Tseng
;  TITLE OF INVENTION: Colon Cancer Antigen Panel
;  FILE REFERENCE: L0461/7105(JRV)
;  CURRENT APPLICATION NUMBER: US/09/849,602
;  CURRENT FILING DATE:  2001-05-04
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-849-602-30

  Query Match             100.0%;  Score 74;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 8
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL-1 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-791-495-7

  Query Match             89.2%;  Score 66;  DB 1;  Length 180;
  Best Local Similarity   92.9%;  Pred. No. 0.25;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              |||||||| |||||
Db         49 GAARASGPRGGAPR 62


RESULT 9
US-09-341-829A-7
; Sequence 7, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-7

  Query Match             89.2%;  Score 66;  DB 2;  Length 180;
  Best Local Similarity   92.9%;  Pred. No. 0.25;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              |||||||| |||||
Db         49 GAARASGPRGGAPR 62


RESULT 10
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL-1 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  210 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-791-495-5

  Query Match             89.2%;  Score 66;  DB 1;  Length 210;
  Best Local Similarity   92.9%;  Pred. No. 0.28;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              |||||||| |||||
Db         49 GAARASGPRGGAPR 62


RESULT 11
US-09-341-829A-5
; Sequence 5, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-5

  Query Match             89.2%;  Score 66;  DB 2;  Length 210;
  Best Local Similarity   92.9%;  Pred. No. 0.28;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              |||||||| |||||
Db         49 GAARASGPRGGAPR 62


RESULT 12
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US-09-252-991A-17335
; Sequence 17335, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 17335
;   LENGTH: 456
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17335

  Query Match             73.0%;  Score 54;  DB 2;  Length 456;
  Best Local Similarity   71.4%;  Pred. No. 18;
  Matches   10;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              || ||:||| | ||
Db        278 GAGRAAGPGTGQPR 291


RESULT 13
US-09-252-991A-24923
; Sequence 24923, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 24923
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24923

  Query Match             70.3%;  Score 52;  DB 2;  Length 210;
  Best Local Similarity   71.4%;  Pred. No. 16;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              | | | | ||||||
Db        157 GTAAADGAGGGAPR 170


RESULT 14
US-09-252-991A-17249
; Sequence 17249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 17249
;   LENGTH: 160
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17249

  Query Match             67.6%;  Score 50;  DB 2;  Length 160;
  Best Local Similarity   69.2%;  Pred. No. 22;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 AARASGPGGGAPR 14
              | | :|||| |||
Db        117 AGRRAGPGGSAPR 129


RESULT 15
US-08-789-329C-10
; Sequence 10, Application US/08789329C
; Patent No. 6165755
;  GENERAL INFORMATION:
;    APPLICANT:  SHERWOOD ET AL.
;    TITLE OF INVENTION:  CHICKEN NEUROPEPTIDE GENE USEFUL
;    TITLE OF INVENTION:  FOR IMPROVED POULTRY PRODUCTION
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klarquist Sparkman Campbell Leigh &
;      ADDRESSEE:  Whinston, LLP
;      STREET:  One World Trade Center
;      STREET:  121 S.W. Salmon Street
;      STREET:  Suite 1600
;      CITY:  Portland
;      STATE:  Oregon
;      COUNTRY:  United States of America
;      ZIP:  97204-2988
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Disk, 3-1/2 inch
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows NT
;      SOFTWARE:  WordPerfect 7.0 & ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/789,329C
;      FILING DATE:  01/23/97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Earp, David J.
;      REGISTRATION NUMBER:  41,401
;      REFERENCE/DOCKET NUMBER:  2847-46468/DJE
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (503) 226-7391
;      TELEFAX:  (503) 228-9446
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  143 aa
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-789-329C-10

  Query Match             66.2%;  Score 49;  DB 2;  Length 143;
  Best Local Similarity   69.2%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 AARASGPGGGAPR 14
              | ||  |||| ||
Db         54 ALRAGAPGGGGPR 66
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Search completed: March 13, 2006, 19:18:51
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:51:56 ; Search time 84.6588 Seconds
(without alignments)
69.096 Million cell updates/sec

Title: US-09-529-206E-27
Perfect score: 74
Sequence: 1 GAARASGPGGGAPR 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	74	100.0	30	4	US-10-296-734-1404	Sequence 1404, Ap
2	74	100.0	179	5	US-10-482-029-202	Sequence 202, App
3	74	100.0	180	3	US-09-751-798-8	Sequence 8, Appli
4	74	100.0	180	3	US-09-849-602-30	Sequence 30, Appl
5	74	100.0	180	4	US-10-023-182-8	Sequence 8, Appli
6	74	100.0	180	4	US-10-207-655-71	Sequence 71, Appl
7	74	100.0	180	4	US-10-364-614-14	Sequence 14, Appl
8	74	100.0	180	4	US-10-026-066-3	Sequence 3, Appli
9	74	100.0	180	4	US-10-117-937-74	Sequence 74, Appl
10	74	100.0	180	4	US-10-295-027-386	Sequence 386, App
11	74	100.0	180	4	US-10-296-734-832	Sequence 832, App
12	74	100.0	180	4	US-10-188-832-139	Sequence 139, App
13	74	100.0	180	4	US-10-777-053-11	Sequence 11, Appl
14	74	100.0	180	4	US-10-751-088-15	Sequence 15, Appl
15	74	100.0	180	4	US-10-657-022-74	Sequence 74, Appl
16	74	100.0	180	4	US-10-837-217-11	Sequence 11, Appl
17	74	100.0	180	5	US-10-877-373-9	Sequence 9, Appli
18	74	100.0	180	5	US-10-723-860-1270	Sequence 1270, Ap
19	74	100.0	180	5	US-10-871-708-7	Sequence 7, Appli
20	74	100.0	180	5	US-10-895-523-3	Sequence 3, Appli
21	74	100.0	180	5	US-10-182-506A-3	Sequence 3, Appli
22	74	100.0	180	5	US-10-756-149-5024	Sequence 5024, Ap
23	74	100.0	180	6	US-11-067-064-74	Sequence 74, Appl
24	74	100.0	180	6	US-11-067-159-74	Sequence 74, Appl
25	74	100.0	397	3	US-09-821-883-27	Sequence 27, Appl
26	74	100.0	397	6	US-11-144-912-27	Sequence 27, Appl
27	74	100.0	3541	4	US-10-296-734-1454	Sequence 1454, Ap
28	66	89.2	30	4	US-10-296-734-1436	Sequence 1436, Ap
29	66	89.2	135	4	US-10-295-027-388	Sequence 388, App
30	66	89.2	135	4	US-10-188-832-141	Sequence 141, App
31	66	89.2	180	4	US-10-146-473-69	Sequence 69, Appl
32	66	89.2	180	4	US-10-117-937-75	Sequence 75, Appl
33	66	89.2	180	4	US-10-296-734-834	Sequence 834, App
34	66	89.2	180	4	US-10-468-406-4	Sequence 4, Appli
35	66	89.2	180	4	US-10-657-022-75	Sequence 75, Appl
36	66	89.2	180	5	US-10-877-373-7	Sequence 7, Appli
37	66	89.2	180	6	US-11-067-064-75	Sequence 75, Appl
38	66	89.2	180	6	US-11-067-159-75	Sequence 75, Appl
39	66	89.2	210	4	US-10-157-031-88	Sequence 88, Appl
40	66	89.2	210	4	US-10-117-937-76	Sequence 76, Appl
41	66	89.2	210	4	US-10-657-022-76	Sequence 76, Appl
42	66	89.2	210	5	US-10-877-373-5	Sequence 5, Appli
43	66	89.2	210	6	US-11-067-064-76	Sequence 76, Appl
44	66	89.2	210	6	US-11-067-159-76	Sequence 76, Appl
45	62	83.8	20	4	US-10-313-986-496	Sequence 496, App

ALIGNMENTS

RESULT 1
US-10-296-734-1404
; Sequence 1404, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1404
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSO1a segment 4
US-10-296-734-1404

Query Match 100.0%; Score 74; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGGAPR 14
||||||||||||||
Db 6 GAARASGPGGGAPR 19

RESULT 2
US-10-482-029-202
; Sequence 202, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-202

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  Query Match             100.0%;  Score 74;  DB 5;  Length 179;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. US20020010321A1
;  GENERAL INFORMATION:
;    APPLICANT:  Stockert, Elisabeth; Jager, Elke;
;    APPLICANT:  Chen, Yao-tseng; Scanlan, Matthew;
;    APPLICANT:  Knuth, Alexander; Old, Lloyd J.
;    TITLE OF INVENTION:  Antibodies Which Bind to NY-ESO-1 Cancer
;    TITLE OF INVENTION:  Associated Proteins, Uses Thereof,
;    TITLE OF INVENTION:  Truncated Forms of NY-ESO-1, and HLA
;    TITLE OF INVENTION:  Binding Peptides Derived Therefrom
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/751,798
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/062,422
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. US20020010321A1man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3168
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-09-751-798-8

  Query Match             100.0%;  Score 74;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 4
US-09-849-602-30
; Sequence 30, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT:  Old, Lloyd J.
;  APPLICANT:  Stockert, Elisabeth
;  APPLICANT:  Chen, Yao-Tseng
;  TITLE OF INVENTION: Colon Cancer Antigen Panel
;  FILE REFERENCE: L0461/7105(JRV)
;  CURRENT APPLICATION NUMBER: US/09/849,602
;  CURRENT FILING DATE:  2001-05-04
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-849-602-30

  Query Match             100.0%;  Score 74;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 5
US-10-023-182-8
; Sequence 8, Application US/10023182
; Publication No. US20020164665A1
;   GENERAL INFORMATION:
;        APPLICANT: Stockert, Elisabeth; Jager, Elke;
;                   Chen, Yao-tseng; Scanlan, Matthew;
;                   Knuth, Alexander; Old, Lloyd J.
;        TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
;                            Associated Proteins, Uses Thereof,
;                            Truncated Forms of NY-ESO-1, and HLA
;                            Binding Peptides Derived Therefrom
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fulbright & Jaworski, L.L.P.
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10103
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: WordPerfect
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/023,182
;             FILING DATE: 17-Dec-2001
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/751,798
;             FILING DATE: December 29, 2000
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/725,182
;             FILING DATE: October 3, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, No. US20020164665A1man D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 5466.3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3168
;             TELEFAX: (212) 752-5958
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 180
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-023-182-8
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  Query Match           100.0%;  Score 74;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 6
US-10-207-655-71
; Sequence 71, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-207-655-71

  Query Match           100.0%;  Score 74;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 7
US-10-364-614-14
; Sequence 14, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
;  APPLICANT: JAGER, Elke
;  APPLICANT:  KNUTH, Alexander
;  APPLICANT:  OLD, Lloyd
;  APPLICANT:  Gnjatic, Sacha
;  TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
;  FILE REFERENCE: LUD 5726.1 CIP
;  CURRENT APPLICATION NUMBER: US/10/364,614
;  CURRENT FILING DATE:  2003-02-24
;  PRIOR APPLICATION NUMBER: US 60/355,828
;  PRIOR FILING DATE: 2002-02-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-364-614-14

  Query Match           100.0%;  Score 74;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 8
US-10-026-066-3
; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
; GENERAL INFORMATION:
;  APPLICANT: Simard, John J. L.
;  APPLICANT:  Diamond, David C.
;  TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
;  TITLE OF INVENTION:  PRESENTING CELLS
;  FILE REFERENCE: CTLIMM.21CP1C
;  CURRENT APPLICATION NUMBER: US/10/026,066
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: 09/561,074
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 09/560,465
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 09/561,572
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 09/561,571
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: PCT/US01/13806
;  PRIOR FILING DATE: 2001-04-27
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-026-066-3

  Query Match           100.0%;  Score 74;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 9
US-10-117-937-74
; Sequence 74, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
;  APPLICANT: CTL IMMUNO THERAPIES CORP.
;  APPLICANT:  SIMARD, John, J.L.
;  APPLICANT:  DIAMOND, David, C.
;  APPLICANT:  LIU, Liping
;  APPLICANT:  XIE, Zhidong
;  TITLE OF INVENTION: EPITOPE SEQUENCES
;  FILE REFERENCE: CTLIMM.027A
;  CURRENT APPLICATION NUMBER: US/10/117,937
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: US 60/282,211
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/337,017
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: US 60/363,210
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 602
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-117-937-74

  Query Match           100.0%;  Score 74;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 10
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US-10-295-027-386
; Sequence 386, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 386
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-386

Query Match 100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGGAPR 14
||||||||||||||
Db 49 GAARASGPGGGAPR 62

RESULT 11
US-10-296-734-832
; Sequence 832, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 832
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYNSO1a consensus polypeptide
US-10-296-734-832

Query Match 100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGGAPR 14
||||||||||||||
Db 49 GAARASGPGGGAPR 62

RESULT 12
US-10-188-832-139
; Sequence 139, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-139

Query Match 100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGGAPR 14
||||||||||||||
Db 49 GAARASGPGGGAPR 62

RESULT 13
US-10-777-053-11
; Sequence 11, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANNK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07

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;  PRIOR APPLICATION NUMBER: 60/336,968
;  PRIOR FILING DATE: 2001-11-07
;  NUMBER OF SEQ ID NOS: 979
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-777-053-11

  Query Match             100.0%;  Score 74;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 14
US-10-751-088-15
; Sequence 15, Application US/10751088
; Publication No. US20040158044A1
;   GENERAL INFORMATION:
;        APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
;                   Gure, Ali, Old, Lloyd, Ritter, Gerd
;        TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                            SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
;                            USES THEREOF
;        NUMBER OF SEQUENCES: 15
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FULBRIGHT & JAWORSKI LLP
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10158
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/751,088
;             FILING DATE: 02-Jan-2004
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/165,546D
;             FILING DATE: 02-Oct-1998
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: April 17, 1998
;             APPLICATION NUMBER: 08/937,263
;             FILING DATE: September 15, 1997
;             APPLICATION NUMBER: US 08/725,182
;             FILING DATE: October 3, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, Norman D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3000
;             TELEFAX: (212) 318-3400
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 180 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-10-751-088-15

  Query Match             100.0%;  Score 74;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


RESULT 15
US-10-657-022-74
; Sequence 74, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
;  APPLICANT: Simard, John J. L.
;  APPLICANT:  Diamond, David C.
;  APPLICANT:  Liu, Liping
;  APPLICANT:  Liu, Zheng
;  TITLE OF INVENTION: EPITOPE SEQUENCES
;  FILE REFERENCE: MANNK.032A
;  CURRENT APPLICATION NUMBER: US/10/657,022
;  CURRENT FILING DATE:  2003-09-04
;  PRIOR APPLICATION NUMBER: 60/409123
;  PRIOR FILING DATE: 2002-09-06
;  NUMBER OF SEQ ID NOS: 610
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-657-022-74

  Query Match             100.0%;  Score 74;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db         49 GAARASGPGGGAPR 62


Search completed: March 13, 2006, 20:02:27
Job time : 85.6588 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:54:06 ; Search time 9.55294 Seconds
(without alignments)
40.793 Million cell updates/sec

Title: US-09-529-206E-27
Perfect score: 74
Sequence: 1 GAARASGPGGGAPR 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	74	100.0	180	7	US-11-155-288-7	Sequence 7, Appli
2	74	100.0	240	7	US-11-021-441-28	Sequence 28, Appl
3	62	83.8	20	6	US-10-623-155-496	Sequence 496, App
4	53	71.6	306	7	US-11-096-568A-20556	Sequence 20556, A
5	53	71.6	353	7	US-11-096-568A-22334	Sequence 22334, A
6	53	71.6	358	7	US-11-096-568A-22333	Sequence 22333, A
7	53	71.6	420	7	US-11-096-568A-22332	Sequence 22332, A
8	47.5	64.2	167	7	US-11-096-568A-10542	Sequence 10542, A
9	46.5	62.8	678	7	US-11-072-512-3295	Sequence 3295, Ap
10	46	62.2	134	7	US-11-096-568A-23806	Sequence 23806, A
11	45.5	61.5	280	7	US-11-143-980-34	Sequence 34, Appl
12	45	60.8	413	7	US-11-096-568A-27265	Sequence 27265, A
13	45	60.8	830	6	US-10-921-793-38	Sequence 38, Appl
14	45	60.8	830	6	US-10-931-198-38	Sequence 38, Appl
15	44	59.5	298	6	US-10-821-234-1240	Sequence 1240, Ap
16	44	59.5	359	7	US-11-096-568A-22662	Sequence 22662, A
17	44	59.5	361	7	US-11-129-143-108	Sequence 108, App
18	44	59.5	368	7	US-11-129-143-107	Sequence 107, App
19	44	59.5	379	7	US-11-109-156-16	Sequence 16, Appl
20	44	59.5	391	7	US-11-096-568A-22661	Sequence 22661, A
21	44	59.5	558	7	US-11-096-568A-26217	Sequence 26217, A
22	44	59.5	974	6	US-10-531-036-35	Sequence 35, Appl
23	43	58.1	113	7	US-11-096-568A-8816	Sequence 8816, Ap
24	43	58.1	155	7	US-11-096-568A-19104	Sequence 19104, A
25	43	58.1	214	6	US-10-892-379-5	Sequence 5, Appli
26	43	58.1	306	7	US-11-096-568A-19986	Sequence 19986, A
27	43	58.1	307	7	US-11-096-568A-19985	Sequence 19985, A
28	43	58.1	314	7	US-11-096-568A-19984	Sequence 19984, A
29	43	58.1	1079	7	US-11-052-554A-145	Sequence 145, App
30	42	56.8	162	7	US-11-096-568A-641	Sequence 641, App
31	42	56.8	169	7	US-11-096-568A-12208	Sequence 12208, A
32	42	56.8	189	7	US-11-107-029-4	Sequence 4, Appli
33	42	56.8	249	7	US-11-096-568A-23045	Sequence 23045, A
34	42	56.8	287	7	US-11-096-568A-25788	Sequence 25788, A
35	42	56.8	293	7	US-11-096-568A-17631	Sequence 17631, A
36	42	56.8	296	7	US-11-096-568A-21195	Sequence 21195, A
37	42	56.8	298	7	US-11-096-568A-25787	Sequence 25787, A
38	42	56.8	304	7	US-11-096-568A-17630	Sequence 17630, A
39	42	56.8	333	7	US-11-096-568A-21193	Sequence 21193, A
40	42	56.8	341	7	US-11-096-568A-25786	Sequence 25786, A
41	42	56.8	360	7	US-11-129-143-113	Sequence 113, App
42	42	56.8	374	7	US-11-129-143-112	Sequence 112, App
43	42	56.8	608	7	US-11-241-347-8	Sequence 8, Appli
44	42	56.8	625	7	US-11-143-984A-39	Sequence 39, Appl
45	42	56.8	625	7	US-11-143-984A-110	Sequence 110, App

ALIGNMENTS

RESULT 1
US-11-155-288-7
; Sequence 7, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-7

Query Match 100.0%; Score 74; DB 7; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGGAPR 14
||||||||||||||
Db 49 GAARASGPGGGAPR 62

RESULT 2
US-11-021-441-28
; Sequence 28, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06

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;  PRIOR APPLICATION NUMBER: US 60/615,287
;  PRIOR FILING DATE: 2004-10-01
;  PRIOR APPLICATION NUMBER: US 60/599,377
;  PRIOR FILING DATE: 2004-08-05
;  PRIOR APPLICATION NUMBER: PCT/US2004/23881
;  PRIOR FILING DATE: 2004-07-23
;  PRIOR APPLICATION NUMBER: US 10/883,599
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: US 60/556,744
;  PRIOR FILING DATE: 2004-03-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion protein
US-11-021-441-28

  Query Match             100.0%;  Score 74;  DB 7;  Length 240;
  Best Local Similarity   100.0%;  Pred. No. 0.0042;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||||||||||||
Db        109 GAARASGPGGGAPR 122


RESULT 3
US-10-623-155-496
; Sequence 496, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Peckham, David W.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C20
;  CURRENT APPLICATION NUMBER: US/10/623,155
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 496
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-623-155-496

  Query Match             83.8%;  Score 62;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.017;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGA 12
              ||||||||||||
Db          9 GAARASGPGGGA 20


RESULT 4
US-11-096-568A-20556
; Sequence 20556, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20556
;   LENGTH: 306
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(306)
;   OTHER INFORMATION: Ceres Seq. ID no. 12383286
US-11-096-568A-20556

  Query Match             71.6%;  Score 53;  DB 7;  Length 306;
  Best Local Similarity   76.9%;  Pred. No. 2.7;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAP 13
              | ||| ||| |||
Db         89 GVARADGPGTGAP 101


RESULT 5
US-11-096-568A-22334
; Sequence 22334, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22334
;   LENGTH: 353
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(353)
;   OTHER INFORMATION: Ceres Seq. ID no. 12408544
US-11-096-568A-22334

  Query Match             71.6%;  Score 53;  DB 7;  Length 353;
  Best Local Similarity   71.4%;  Pred. No. 3.1;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||  ||||  ||
Db        107 GAARGQGPGGEQPR 120


RESULT 6
US-11-096-568A-22333
; Sequence 22333, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22333
;   LENGTH: 358
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(358)
;   OTHER INFORMATION: Ceres Seq. ID no. 12408543
US-11-096-568A-22333

  Query Match             71.6%;  Score 53;  DB 7;  Length 358;
  Best Local Similarity   71.4%;  Pred. No. 3.1;
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  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||  ||||  ||
Db        112 GAARGQGPGGEQPR 125


RESULT 7
US-11-096-568A-22332
; Sequence 22332, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22332
;   LENGTH: 420
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(420)
;   OTHER INFORMATION: Ceres Seq. ID no. 12408542
US-11-096-568A-22332

  Query Match            71.6%;  Score 53;  DB 7;  Length 420;
  Best Local Similarity  71.4%;  Pred. No. 3.6;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              ||||  ||||  ||
Db        174 GAARGQGPGGEQPR 187


RESULT 8
US-11-096-568A-10542
; Sequence 10542, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 10542
;   LENGTH: 167
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(167)
;   OTHER INFORMATION: Ceres Seq. ID no. 13596390
US-11-096-568A-10542

  Query Match            64.2%;  Score 47.5;  DB 7;  Length 167;
  Best Local Similarity  73.3%;  Pred. No. 8.3;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 GAARASGP-GGGAPR 14
              |||   || ||||||
Db         92 GAAPGRGPRGGGAPR 106


RESULT 9
US-11-072-512-3295
; Sequence 3295, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
;  APPLICANT: ISOGAI, TAKAO
;  APPLICANT:  SUGIYAMA, TOMOYASU
;  APPLICANT:  OTSUKI, TETSUJI
;  APPLICANT:  WAKAMATSU, AI
;  APPLICANT:  SATO, HIROYUKI
;  APPLICANT:  ISHII, SHIZUKO
;  APPLICANT:  YAMAMOTO, JUN-ICHI
;  APPLICANT:  ISONO, YUUKO
;  APPLICANT:  HIO, YURI
;  APPLICANT:  OTSUKA, KAORU
;  APPLICANT:  NAGAI, KEIICHI
;  APPLICANT:  IRIE, RYOTARO
;  APPLICANT:  TAMECHIKA, ICHIRO
;  APPLICANT:  SEKI, NAOHIKO
;  APPLICANT:  YOSHIKAWA, TSUTOMU
;  APPLICANT:  OTSUKA, MOTOYUKI
;  APPLICANT:  NAGAHARI, KENJI
;  APPLICANT:  MASUHO, YASUHIKO
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: 084335-0191
;  CURRENT APPLICATION NUMBER: US/11/072,512
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: US 60/350,978
;  PRIOR FILING DATE: 2002-01-25
;  PRIOR APPLICATION NUMBER: JP 2001-379298
;  PRIOR FILING DATE: 2001-11-05
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3295
;   LENGTH: 678
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-072-512-3295

  Query Match            62.8%;  Score 46.5;  DB 7;  Length 678;
  Best Local Similarity  61.1%;  Pred. No. 38;
  Matches   11;  Conservative    1;  Mismatches    1;  Indels    5;  Gaps    1;

Qy          1 GAA-----RASGPGGGAP 13
              |||     ||:||||| |
Db        584 GAAKPPRPRAAGPGGGWP 601


RESULT 10
US-11-096-568A-23806
; Sequence 23806, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23806
;   LENGTH: 134
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(134)
;   OTHER INFORMATION: Ceres Seq. ID no. 12415289
US-11-096-568A-23806

  Query Match            62.2%;  Score 46;  DB 7;  Length 134;
  Best Local Similarity  72.7%;  Pred. No. 11;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 ARASGPGGGAP 13
              || :||| |||
Db         69 ARGAGPGAGAP 79
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```
RESULT 11
US-11-143-980-34
; Sequence 34, Application US/11143980
; Publication No. US20050272133A1
; GENERAL INFORMATION:
;  APPLICANT: He, Min
;  APPLICANT:  Hucul, John
;  APPLICANT:  Haltli, Bradley A.
;  APPLICANT:  Wagenaar, Melissa M.
;  APPLICANT:  Graziani, Edmund
;  APPLICANT:  Summers, Mia
;  APPLICANT:  Kulowski, Kerry
;  APPLICANT:  Pong, Kevin
;  TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex
;  TITLE OF INVENTION:  Polyketide
;  FILE REFERENCE: AM-101426US
;  CURRENT APPLICATION NUMBER: US/11/143,980
;  CURRENT FILING DATE:  2005-06-03
;  PRIOR APPLICATION NUMBER: US 60/664,483
;  PRIOR FILING DATE: 2005-03-23
;  PRIOR APPLICATION NUMBER: US 60/576,895
;  PRIOR FILING DATE: 2004-06-03
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
;   LENGTH: 280
;   TYPE: PRT
;   ORGANISM: Streptomyces sp.
US-11-143-980-34

  Query Match             61.5%;  Score 45.5;  DB 7;  Length 280;
  Best Local Similarity   66.7%;  Pred. No. 24;
  Matches   10;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 GAARASGPGG-GAPR 14
              |: | ||||| | ||
Db        113 GSNRPSQPGGPGGPR 127


RESULT 12
US-11-096-568A-27265
; Sequence 27265, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27265
;   LENGTH: 413
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(413)
;   OTHER INFORMATION: Ceres Seq. ID no. 15180691
US-11-096-568A-27265

  Query Match             60.8%;  Score 45;  DB 7;  Length 413;
  Best Local Similarity   64.3%;  Pred. No. 39;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGAPR 14
              | || :|||| | |
Db         61 GVARLAGPGGRAGR 74


RESULT 13
US-10-921-793-38
; Sequence 38, Application US/10921793
; Publication No. US20060039949A1
; GENERAL INFORMATION:
;  APPLICANT: Nycz, Jeffrey
;  TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated
;  TITLE OF INVENTION:  Osteoinductive Material
;  FILE REFERENCE: 64118.000087
;  CURRENT APPLICATION NUMBER: US/10/921,793
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 830
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-921-793-38

  Query Match             60.8%;  Score 45;  DB 6;  Length 830;
  Best Local Similarity   66.7%;  Pred. No. 72;
  Matches    8;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGA 12
              |:| |:||| ||
Db        673 GSAEAAGPGAGA 684


RESULT 14
US-10-931-198-38
; Sequence 38, Application US/10931198
; Publication No. US20060045902A1
; GENERAL INFORMATION:
;  APPLICANT: Nycz, Jeffrey
;  TITLE OF INVENTION: Orthopaedic Device with Porous Substrate and Impregnated
;  TITLE OF INVENTION:  Osteoinductive Material
;  FILE REFERENCE: 64118.000087
;  CURRENT APPLICATION NUMBER: US/10/931,198
;  CURRENT FILING DATE:  2004-09-01
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 830
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-931-198-38

  Query Match             60.8%;  Score 45;  DB 6;  Length 830;
  Best Local Similarity   66.7%;  Pred. No. 72;
  Matches    8;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GAARASGPGGGA 12
              |:| |:||| ||
Db        673 GSAEAAGPGAGA 684


RESULT 15
US-10-821-234-1240
; Sequence 1240, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1240
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; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1240

Query Match 59.5%; Score 44; DB 6; Length 298;
Best Local Similarity 64.3%; Pred. No. 39;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 GAARASGPGGGAPR 14
              | ||  |||  |||
Db        133 GPARPLGPGPAAPR 146
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Search completed: March 13, 2006, 20:03:30
Job time : 9.55294 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 18:52:59 ; Search time 97.8824 Seconds
(without alignments)
58.355 Million cell updates/sec

Title: US-09-529-206E-28
Perfect score: 68
Sequence: 1 AARASGPGGGAPR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
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4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	68	100.0	13	2	AAY06064	Aay06064 Human can
2	68	100.0	14	2	AAY05986	Aay05986 Human can
3	68	100.0	15	2	AAY05978	Aay05978 Human can
4	68	100.0	20	2	AAY05979	Aay05979 Human can
5	68	100.0	30	5	AAU85105	Aau85105 Human NYN
6	68	100.0	179	8	ADK68648	Adk68648 Epitope 1
7	68	100.0	180	2	AAW62584	Aaw62584 Cancer as
8	68	100.0	180	2	AAW69665	Aaw69665 Human NY-
9	68	100.0	180	2	AAY05965	Aay05965 Human can
10	68	100.0	180	3	AAY52430	Aay52430 Human tum
11	68	100.0	180	3	AAY70862	Aay70862 Human tum
12	68	100.0	180	3	AAB03154	Aab03154 Human oes
13	68	100.0	180	4	AAB69946	Aab69946 Human NY-
14	68	100.0	180	4	AAG67164	Aag67164 Amino aci
15	68	100.0	180	4	AAU01535	Aau01535 Human NY-
16	68	100.0	180	4	AAE07714	Aae07714 Human NY
17	68	100.0	180	5	AAU84818	Aau84818 Human NYN
18	68	100.0	180	5	AAU11543	Aau11543 Human tum
19	68	100.0	180	6	ABR58672	Abr58672 Human can
20	68	100.0	180	6	ABR48210	Abr48210 Human bla
21	68	100.0	180	6	ABU56508	Abu56508 Lung canc
22	68	100.0	180	6	ABU56694	Abu56694 Lung canc
23	68	100.0	180	6	ABP74198	Abp74198 Human NY-
24	68	100.0	180	6	ABU64816	Abu64816 Human NY-
25	68	100.0	180	6	ABR83438	Abr83438 Human NY-
26	68	100.0	180	7	ADC09576	Adc09576 NY-ESO-1
27	68	100.0	180	7	ADD35564	Add35564 Human NY-
28	68	100.0	180	7	ADD35568	Add35568 Human NY-
29	68	100.0	180	7	ADD25510	Add25510 Binding d
30	68	100.0	180	7	ADN39068	Adn39068 Cancer/an
31	68	100.0	180	8	ADJ54139	Adj54139 Human NY-
32	68	100.0	180	8	ADM72815	Adm72815 Human NY-
33	68	100.0	180	8	ADM73418	Adm73418 CAG-3 pro
34	68	100.0	180	8	ADM73417	Adm73417 Human NY-
35	68	100.0	180	8	ADQ18451	Adq18451 Human sof
36	68	100.0	180	8	ADQ10446	Adq10446 Autoimmun
37	68	100.0	180	8	ADS80926	Ads80926 Tumour as
38	68	100.0	180	9	ADW44353	Adw44353 Human aut
39	68	100.0	180	9	ADY85096	Ady85096 Tumor ant
40	68	100.0	180	9	ADZ28913	Adz28913 NY-ESO-1
41	68	100.0	180	9	ADZ42374	Adz42374 Immunogen
42	68	100.0	180	9	AEA35651	Aea35651 Human NY-
43	68	100.0	240	9	ADW99402	Adw99402 NY-ESO-1/
44	68	100.0	240	9	AEB80047	Aeb80047 Human NY-
45	68	100.0	397	4	AAE13122	Aae13122 NY-ESO-IC

ALIGNMENTS

RESULT 1
AAY06064
ID AAY06064 standard; peptide; 13 AA.
XX
AC AAY06064;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 peptide.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Example 11; Page 50; 88pp; English.
XX
CC This peptide corresponds to amino acid residues 50-62 of human NY ESO-
CC 1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is
CC capable of eliciting an antigen specific immune response by T cells.
CC Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3
CC and their variants, are useful as cancer vaccines. A claimed method of
CC preventing or inhibiting cancer involves administering a cancer peptide,
CC with or without an HLA molecule. The cancer peptides form part of, or are
CC derived from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,

```
CC   cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC   as breast, prostate, ovarian, pancreatic and thyroid cancers
XX
SQ   Sequence 13 AA;

  Query Match             100.0%;  Score 68;  DB 2;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0.017;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db          1 AARASGPGGGAPR 13


RESULT 2
AAY05986
ID   AAY05986 standard; peptide; 14 AA.
XX
AC   AAY05986;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
KW   NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW   leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW   metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW   uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW   cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW   liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW   vaccine.
XX
OS   Homo sapiens.
XX
PN   WO9918206-A2.
XX
PD   15-APR-1999.
XX
PF   21-SEP-1998;   98WO-US019609.
XX
PR   08-OCT-1997;   97US-0061428P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang RF,  Rosenberg SA;
XX
DR   WPI; 1999-277270/23.
XX
PT   Cancer antigen NY ESO1/CAG-3.
XX
PS   Claim 25; Page 50; 88pp; English.
XX
CC   The present sequence represents a cancer peptide that corresponds to
CC   amino acid residues 49-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
CC   AAY05965), a new and potent tumour antigen capable of eliciting an
CC   antigen specific immune response by T cells. Cancer peptides derived from
CC   CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
CC   variants (see AAY05967-87), are useful as cancer vaccines that protect
CC   against cancer. The invention provides: vectors and host cells (also
CC   useful as vaccines); a method of diagnosis of cancer or precancer; a
CC   transgenic animal; antisense oligonucleotides that inhibit expression of
CC   the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
CC   cancer peptide, useful in diagnostic and detection assays; and methods
CC   for preventing or inhibiting cancer by administering a cancer peptide,
CC   with or without an HLA molecule. The cancer peptides form part of, or are
CC   derived from, cancers such as primary or metastatic melanoma, thymoma,
CC   lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC   cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC   as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
CC   treated by inducing cancer-specific T cells in vitro for subsequent
CC   return to a patient
XX
SQ   Sequence 14 AA;

  Query Match             100.0%;  Score 68;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0.018;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db          2 AARASGPGGGAPR 14


RESULT 3
AAY05978
ID   AAY05978 standard; peptide; 15 AA.
XX
AC   AAY05978;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
KW   NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW   leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW   metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW   uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW   cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW   liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW   vaccine.
XX
OS   Homo sapiens.
XX
PN   WO9918206-A2.
XX
PD   15-APR-1999.
XX
PF   21-SEP-1998;   98WO-US019609.
XX
PR   08-OCT-1997;   97US-0061428P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang RF,  Rosenberg SA;
XX
DR   WPI; 1999-277270/23.
XX
PT   Cancer antigen NY ESO1/CAG-3.
XX
PS   Claim 15; Page 64; 88pp; English.
XX
CC   The present sequence represents a cancer peptide that corresponds to
CC   amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
CC   AAY05965), a new and potent tumour antigen capable of eliciting an
CC   antigen specific immune response by T cells. Cancer peptides derived from
CC   CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
CC   variants (see AAY05967-87), are useful as cancer vaccines that protect
CC   against cancer. The invention provides: vectors and host cells (also
CC   useful as vaccines); a method of diagnosis of cancer or precancer; a
CC   transgenic animal; antisense oligonucleotides that inhibit expression of
CC   the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
CC   cancer peptide, useful in diagnostic and detection assays; and methods
CC   for preventing or inhibiting cancer by administering a cancer peptide,
CC   with or without an HLA molecule. The cancer peptides form part of, or are
CC   derived from, cancers such as primary or metastatic melanoma, thymoma,
CC   lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC   cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC   as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
CC   treated by inducing cancer-specific T cells in vitro for subsequent
CC   return to a patient
XX
SQ   Sequence 15 AA;

  Query Match             100.0%;  Score 68;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db          3 AARASGPGGGAPR 15


RESULT 4
AAY05979
ID   AAY05979 standard; peptide; 20 AA.
XX
AC   AAY05979;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
KW   NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW   leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW   metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW   uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW   cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW   liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW   vaccine.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9918206-A2.
XX
PD   15-APR-1999.
XX
PF   21-SEP-1998;   98WO-US019609.
XX
PR   08-OCT-1997;   97US-0061428P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang RF,  Rosenberg SA;
XX
DR   WPI; 1999-277270/23.
XX
PT   Cancer antigen NY ESO1/CAG-3.
XX
PS   Claim 16; Page 64; 88pp; English.
XX
CC   The present sequence represents a cancer peptide that is based on amino
CC   acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965),
CC   a new and potent tumour antigen capable of eliciting an antigen specific
CC   immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-
CC   3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-
CC   87), are useful as cancer vaccines that protect against cancer. The
CC   invention provides: vectors and host cells (also useful as vaccines); a
CC   method of diagnosis of cancer or precancer; a transgenic animal;
CC   antisense oligonucleotides that inhibit expression of the cancer peptide
CC   or tumour antigen; antibodies reacting with a CAG-3 cancer peptide,
CC   useful in diagnostic and detection assays; and methods for preventing or
CC   inhibiting cancer by administering a cancer peptide, with or without an
CC   HLA molecule. The cancer peptides form part of, or are derived from,
CC   cancers such as primary or metastatic melanoma, thymoma, lymphoma,
CC   sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
CC   cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
CC   prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by
CC   inducing cancer-specific T cells in vitro for subsequent return to a
CC   patient
XX
SQ   Sequence 20 AA;

  Query Match             100.0%;  Score 68;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.024;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db          8 AARASGPGGGAPR 20


RESULT 5
AAU85105
ID   AAU85105 standard; peptide; 30 AA.
XX
AC   AAU85105;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Human NYNSO1a segment 4.
XX
KW   Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW   viral infection; human immunodeficieny virus; melanoma;
KW   bacterial infection; Salmonella; Legionella; parasitic infection;
KW   Trypanosoma; Toxoplasma; Giardia.
XX
OS   Homo sapiens.
XX
PN   WO200190197-A1.
XX
PD   29-NOV-2001.
XX
PF   25-MAY-2001; 2001WO-AU000622.
XX
PR   26-MAY-2000; 2000AU-00007761.
XX
PA   (AUSU ) UNIV AUSTRALIAN NAT.
XX
PI   Thomson SA,  Ramshaw IA;
XX
DR   WPI; 2002-147575/19.
DR   N-PSDB; ABK36925.
XX
PT   New synthetic polypeptides having several different segments of at least
PT   one parent polypeptide linked together differently compared to the
PT   linkage in the parent polypeptide, for inducing immune response against a
PT   pathogen or cancer.
XX
PS   Example 3; Fig 27; 364pp; English.
XX
CC   The invention relates to a new synthetic polypeptide (I) comprising
CC   several different segments of at least one parent polypeptide linked
CC   together in a different relationship relative to their linkage in the
CC   parent polypeptide to impede, abrogate or otherwise alter at least one
CC   function associated with the parent polypeptide and for inducing an
CC   immune response against a pathogen or cancer. Also included are a
CC   synthetic polynucleotide encoding and a computer system for designing the
CC   synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC   are referred to as a Savine. The synthetic polypeptide is useful for
CC   modulating immune responses preferably directed against a pathogen or a
CC   cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC   and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC   oesophagus, brain, testicle, uterus), as potentiating agents.
CC   Compositions comprising the polypeptide may be used in the treatment or
CC   prophylaxis against viral (such as infections caused by HIV (human
CC   immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC   virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC   (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC   Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC   (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC   Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC   a peptide derived from a parent protein used to construct a savine of the
CC   invention
XX
SQ   Sequence 30 AA;

  Query Match             100.0%;  Score 68;  DB 5;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.034;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
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                ||||||||||||
Db          7 AARASGPGGGAPR 19


RESULT 6
ADK68648
ID   ADK68648 standard; protein; 179 AA.
XX
AC   ADK68648;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Epitope liberation-related NY-ESO-1 protein SeqID11.
XX
KW   epitope liberation; substrate; proteasome; cytostatic; antibacterial;
KW   protozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope;
KW   cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;
KW   virus; bacterium; protozoan; fungus; housekeeping proteasome system;
KW   human.
XX
OS   Homo sapiens.
XX
PN   US2003228634-A1.
XX
PD   11-DEC-2003.
XX
PF   07-NOV-2002; 2002US-00292413.
XX
PR   07-NOV-2001; 2001US-0336968P.
XX
PA   (SIMA/) SIMARD J J L.
PA   (DIAM/) DIAMOND D C.
PA   (QIUZ/) QIU Z.
PA   (LEIX/) LEI X.
XX
PI   Simard JJL,  Diamond DC,  Qiu Z,  Lei X;
XX
DR   WPI; 2004-167209/16.
DR   N-PSDB; ADK68674.
XX
PT   Identifying polypeptide suitable for epitope e.g., housekeeping epitope,
PT   liberation by contacting substrate polypeptide comprising epitope of
PT   interest, with proteasome, and assaying for liberation of epitope.
XX
PS   Example 2; SEQ ID NO 11; 67pp; English.
XX
CC   This invention relates to a novel method of identifying a polypeptide
CC   suitable for epitope liberation, including the steps of identifying an
CC   epitope of interest; providing substrate polypeptide sequence including
CC   the epitope, wherein the substrate permits processing by a proteasome;
CC   contacting the substrate with a composition including the proteasome,
CC   under conditions that support processing of the substrate by proteasome;
CC   and assaying for liberation of epitope. The invention may be useful for
CC   the development of compounds with a cytostatic, antibacterial,
CC   protozoacide or fungicide activity acting as T-cell activators. In
CC   addition, the invention may allow development of a vaccine. The invention
CC   is useful for identifying a polypeptide suitable for epitope liberation,
CC   where the epitope is a housekeeping epitope. The compositions comprising
CC   the identified housekeeping epitopes are useful in vitro in vaccine
CC   development or in the generation or expansion of cytotoxic T lymphocyte
CC   (CTL) to be used in adoptive immunotherapy. The invention is also useful
CC   for activating T-cells against neoplastic cells, and cells infected with
CC   virus, bacterium, protozoan or fungus. CTL epitopes are identified based
CC   on the knowledge that such epitopes are, in fact, produced by the
CC   housekeeping proteasome system. Once identified, these epitopes, embodied
CC   as peptides, can be used to successfully immunise or induce therapeutic
CC   CTL responses against housekeeping proteasome expressing target cells in
CC   the host. The present sequence is that of a protein which is related to
CC   the method of the invention.
XX
SQ   Sequence 179 AA;

  Query Match             100.0%;  Score 68;  DB 8;  Length 179;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         49 AARASGPGGGAPR 61


RESULT 7
AAW62584
ID   AAW62584 standard; protein; 180 AA.
XX
AC   AAW62584;
XX
DT   17-SEP-1998  (first entry)
XX
DE   Cancer associated antigen NY-ESO-1.
XX
KW   Cancer associated antigen; NY-ESO-1; regression; progression; onset;
KW   cancer; treatment; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 7
FT                   /note= "potential myristorylation site"
FT   Misc-difference 9
FT                   /note= "potential myristorylation site"
FT   Misc-difference 11
FT                   /note= "potential phosphorylation site"
FT   Misc-difference 98
FT                   /note= "potential phosphorylation site"
FT   Misc-difference 134
FT                   /note= "potential phosphorylation site"
FT   Misc-difference 138
FT                   /note= "potential phosphorylation site"
XX
PN   WO9814464-A1.
XX
PD   09-APR-1998.
XX
PF   15-SEP-1997;   97WO-US016335.
XX
PR   03-OCT-1996;   96US-00725182.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Chen Y,  Scanlan M,  Gure A,  Old LJ,  Jager E,  Knuth A;
PI   Drijfhout JW;
XX
DR   WPI; 1998-286417/25.
DR   N-PSDB; AAV38566.
XX
PT   New isolated cancer associated antigen - is used to develop products for
PT   the diagnosis and treatment of cancers and for monitoring cancer therapy.
XX
PS   Claim 8; Fig 3; 49pp; English.
XX
CC   The present sequence represents a cancer associated antigen. The clone
CC   from which the DNA sequence is obtained is designated NY-ESO-1. The
CC   specification described a method for determining regression, progression
CC   of onset of a cancerous condition, comprising monitoring a sample from a
CC   patient with the cancerous condition for a parameter selected from NY-ESO
CC   -1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells
CC   specific for the peptide and an MHC molecule with which it non-covalently
CC   complexes. Methods for the treatment of a cancerous condition are also
CC   described. The NY-ESO-1 protein and peptides derived from it can be used
CC   for diagnosis and treatment of cancers and to monitor the efficacy of a
CC   therapeutic regime
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 68;  DB 2;  Length 180;
```

```
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62


RESULT 8
AAW69665
ID   AAW69665 standard; protein; 180 AA.
XX
AC   AAW69665;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
XX
KW   Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
XX
OS   Homo sapiens.
XX
PN   WO9832855-A1.
XX
PD   30-JUL-1998.
XX
PF   27-JAN-1998;   98WO-US001445.
XX
PR   27-JAN-1997;   97US-00791495.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Lethe B,  Lucas S,  De Smet C,  Godelaine D,  Boon-Falleur T;
XX
DR   WPI; 1998-427951/36.
DR   N-PSDB; AAV50348.
XX
PT   New isolated LAGE-1 tumour associated nucleic acids - used to develop
PT   products for the diagnosis and treatment of LAGE-1 associated disorders,
PT   particularly tumours.
XX
PS   Example 2; Page 57-58; 73pp; English.
XX
CC   The present sequence represents human NY-ESO-1, formerly known as LL-1.2
CC   clone, which is used in an example from the present invention which
CC   describes LAGE-1 tumour associated protein (TAP). The present invention
CC   also describes: (1) a method for treating a subject with a disorder
CC   characterised by expression of a LAGE-1 nucleic acid molecule or an
CC   expression product, comprising administering to the subject autologous
CC   cytolytic T cells to ameliorate the disorder, where the cytolytic T cells
CC   are specific for complexes of an HLA molecule and a LAGE-1 TAP or an
CC   immunogenic fragment; (2) a method for treating a subject with a disorder
CC   characterised by expression of a LAGE-1 nucleic acid molecule or an
CC   expression product, comprising administering a LAGE-1 TAP or an
CC   immunogenic fragment to ameliorate the disorder; and (3) a method for
CC   selectively enriching a population of T cells with cytolytic T cells
CC   specific for a LAGE-1 TAP comprising contacting an isolated population of
CC   T cells with an agent presenting a complex of a LAGE TAP or an
CC   immunogenic fragment and a HLA presenting molecule to selectively enrich
CC   the isolated population of T cells with the cytolytic T cells. The
CC   methods and products from the present invention can be used for the
CC   diagnosis and treatment of LAGE-1 associated disorders, particularly
CC   tumours
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 68;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62


RESULT 9
AAY05965
ID   AAY05965 standard; protein; 180 AA.
XX
AC   AAY05965;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.
XX
KW   NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia;
KW   non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis;
KW   melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer;
KW   breast cancer; prostate cancer; ovarian cancer; cervical cancer;
KW   bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma;
KW   tumour; diagnosis; immunotherapy; therapy; vaccine; ORF1.
XX
OS   Homo sapiens.
XX
PN   WO9918206-A2.
XX
PD   15-APR-1999.
XX
PF   21-SEP-1998;   98WO-US019609.
XX
PR   08-OCT-1997;   97US-0061428P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang RF,  Rosenberg SA;
XX
DR   WPI; 1999-277270/23.
DR   N-PSDB; AAX58599.
XX
PT   Cancer antigen NY ESO1/CAG-3.
XX
PS   Claim 4; Fig 3A; 88pp; English.
XX
CC   The present sequence represents the ORF1 protein encoded by open reading
CC   frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and
CC   potent tumour antigen capable of eliciting an antigen specific immune
CC   response by T cells. Cancer peptides comprising ORF1, ORF2 (see
CC   AAY05966), portions of these peptides and their variants (see AAY05965-
CC   87), are useful as cancer vaccines that protect the recipient from
CC   development of cancer. The invention provides: vectors and host cells
CC   (also useful as vaccines); a method of diagnosis of cancer or precancer;
CC   a transgenic animal; antisense oligonucleotides that inhibit expression
CC   of the cancer peptide or tumour antigen; antibodies reacting with the CAG
CC   -3 cancer peptide, useful in diagnostic and detection assays; and methods
CC   for preventing or inhibiting cancer by administering a cancer peptide,
CC   with or without an HLA molecule. The cancer peptides form part of, or are
CC   derived from, cancers such as primary or metastatic melanoma, thymoma,
CC   lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC   cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC   as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
CC   treated by inducing cancer-specific T cells in vitro for subsequent
CC   return to a patient
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 68;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62


RESULT 10
AAY52430
```

```
ID   AAY52430 standard; protein; 180 AA.
XX
AC   AAY52430;
XX
DT   21-OCT-2004  (revised)
DT   15-FEB-2000  (first entry)
XX
DE   Human tumour antigen NY-ESO-1.
XX
KW   Cancer; tumour; antigen; MHC; major histocompatility complex; T-cell;
KW   cytotoxic; helper; stimulation; proliferation; treatment; diagnosis;
KW   prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;
KW   hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Peptide         44. .53
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         60. .69
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         60. .68
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         63. .72
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         79. .88
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         79. .87
FT                   /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
FT                   and HLA-B35"
FT   Peptide         82. .91
FT                   /note= "Peptide presented by MHC Class I HLA-A1"
FT   Peptide         82. .90
FT                   /note= "Peptide presented by MHC Class I HLA-A1"
FT   Peptide         83. .91
FT                   /note= "Peptide presented by MHC Class I HLA-B44"
FT   Peptide         84. .92
FT                   /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
FT                   and HLA-B35"
FT   Peptide         87. .96
FT                   /note= "Peptide presented by MHC Class I HLA-A1"
FT   Peptide         88. .96
FT                   /note= "Peptide presented by MHC Class I HLA-B44"
FT   Peptide         96. .104
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         100. .108
FT                   /note= "Peptide presented by MHC Class I HLA-B44"
FT   Peptide         102. .110
FT                   /note= "Peptide presented by MHC Class I HLA-B44"
FT   Peptide         107. .116
FT                   /note= "Peptide presented by MHC Class I HLA-A24"
FT   Peptide         110. .118
FT                   /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide         113. .122
FT                   /note= "Peptide presented by MHC Class I HLA-B7 and HLA-
FT                   B52"
FT   Peptide         113. .121
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         115. .124
FT                   /note= "Peptide presented by MHC Class I HLA-A3"
FT   Peptide         118. .126
FT                   /note= "Peptide presented by MHC Class I HLA-B35"
FT   Peptide         124. .133
FT                   /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide         125. .133
FT                   /note= "Peptide presented by MHC Class I HLA-A24"
FT   Peptide         138. .147
FT                   /note= "Peptide presented by MHC Class I HLA-B8"
FT   Peptide         139. .147
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         145. .153
FT                   /note= "Peptide presented by MHC Class I HLA-A24 and HLA-
FT                   B52"
FT   Peptide         153. .162
FT                   /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide         154. .163
FT                   /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide         154. .162
FT                   /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide         156. .167
FT                   /note= "Peptide (AAY52434) presented by MHC Class I HLA-
FT                   A2"
FT   Peptide         158. .166
FT                   /note= "Peptide presented by MHC Class I HLA-A3"
FT   Peptide         159. .167
FT                   /note= "Peptide presented by MHC Class I HLA-A3"
FT   Peptide         162. .170
FT                   /note= "Peptide presented by MHC Class I HLA-B52"
XX
PN   WO9953938-A1.
XX
PD   28-OCT-1999.
XX
PF   24-MAR-1999;   99WO-US006875.
XX
PR   17-APR-1998;   98US-00062422.
PR   02-OCT-1998;   98US-00165546.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Stockert E,  Jager E,  Chen Y,  Scanlan M,  Alexander K,  Old LJ;
PI   Gure A,  Ritter G;
XX
DR   WPI; 2000-038483/03.
DR   N-PSDB; AAZ38380.
XX
PT   Novel peptides which bind to MHC class I and MHC class II molecules,
PT   useful for therapeutic and diagnostic purposes.
XX
PS   Claim 30; Fig 3; 49pp; English.
XX
CC   This sequence represents a human tumour antigen, NY-ESO-1, the cDNA
CC   encoding which was isolated from an oesophagus squamous cell cancer cDNA
CC   library. Tissue localisation studies revealed it to be expressed at high
CC   levels in normal ovary and testis but not in normal colon, kidney, liver,
CC   brain, oesophagus and skin. It was expressed in certain tumours and
CC   tumour cell lines with some degree of frequency - these included melanoma
CC   specimens and cell lines, and breast and bladder cancer specimens, with
CC   expression in other tumour types being sporadic. Peptides derived from NY
CC   -ESO-1 are bound by both MHC (major histocompatibility complex) Class I
CC   and Class II molecules for presentation to T-cells. Peptides AAY52431-
CC   Y52434 bind to Class I HLA-A2 molecules, thereby stimulating
CC   proliferation of cytotoxic T-cells, while peptides AAY52435-Y52440 bind
CC   to Class II HLA-DR53 molecules, stimulating helper T-cell proliferation.
CC   The peptides derived from NY-ESO-1 may be used in methods and
CC   compositions used for the treatment, diagnosis and prevention of cancers
CC   (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma,
CC   ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to
CC   stimulate the proliferation of T cells
CC
CC   Revised record issued on 21-OCT-2004 : Correction to feature table key
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 68;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62


RESULT 11
AAY70862
```

ID AAY70862 standard; protein; 180 AA.
XX
AC AAY70862;
XX
DT 31-JUL-2000 (first entry)
XX
DE Human tumour antigen, NY-ESO-1 protein.
XX
KW NY-ESO-1; CAMEL; CTL-recognised Antigen on MELanoma; human; cancer; CTL;
KW cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer;
KW melanoma; immunotherapy; immune response.
XX
OS Homo sapiens.
XX
PN WO200023584-A1.
XX
PD 27-APR-2000.
XX
PF 15-OCT-1999; 99WO-EP007832.
XX
PR 16-OCT-1998; 98EP-00119583.
XX
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (UYHO-) UNIV HOSPITAL LEIDEN.
XX
PI Schrier PI, Aarnoudse CA, Heider K, Klade C;
XX
DR WPI; 2000-339685/29.
DR N-PSDB; AAD00152.
XX
PT Tumor-associated antigen useful for cancer immunotherapy is encoded by
PT the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
XX
PS Example 3; Page 62-63; 73pp; English.
XX
CC The present sequence is the human NY-ESO-1 protein, a tumour antigen,
CC identified by screening an esophagus carcinoma cDNA library. This protein
CC is derived from open reading frame (ORF)-1 that contain epitopes of
CC tumour specific T-cells. NY-ESO-1 is expressed in different tumour types,
CC but not in healthy tissues except in testis. It also shows homology with
CC the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELanoma)
CC protein, a tumour-asociated antigen. The tumour-associated antigen
CC displayed on melanoma cells is recognised by cytotoxic T lymphocytes.
CC This sequence has anticancer activity. CAMEL tumour antigen and
CC immunogenic peptides derived from it are useful for cancer immunotherapy.
CC They have the potential to induce an immune response, by eliciting a CTL
CC response. The DNA molecule is used for the construction of recombinant or
CC fusion proteins
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 68; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AARASGPGGGAPR 13
||||||||||||
Db 50 AARASGPGGGAPR 62

RESULT 12
AAB03154
ID AAB03154 standard; protein; 180 AA.
XX
AC AAB03154;
XX
DT 23-OCT-2000 (first entry)
XX
DE Human oesophageal cancer-associated antigen NY-ESO-1.
XX
KW Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen;
KW oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain;
KW antibody; diagnostic marker; drug delivery target.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 7
FT /note= "Potential N-myristoylation site"
FT Modified-site 9
FT /note= "Potential N-myristoylation site"
FT Modified-site 11
FT /note= "Potential O-phosphorylation site"
FT Modified-site 98
FT /note= "Potential O-phosphorylation site"
FT Modified-site 134
FT /note= "Potential O-phosphorylation site"
FT Modified-site 138
FT /note= "Potential O-phosphorylation site"
FT Domain 152. .172
FT /note= "Potential transmembrane domain"
XX
PN US6069233-A.
XX
PD 30-MAY-2000.
XX
PF 26-JAN-1998; 98US-00013150.
XX
PR 03-OCT-1996; 96US-00725381.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Scanlan M, Gure AO, Chen Y, Tureci O, Sahin U, Pfreundschuh M;
PI Old LJ;
XX
DR WPI; 2000-410880/35.
DR N-PSDB; AAA61483.
XX
PT New isolated esophageal cancer-associated antigen useful as markers for
PT producing antibodies and as targets for identifying abnormal conditions,
PT e.g. infections and cancer.
XX
PS Example 5; Fig 3; 9pp; English.
XX
CC This sequence represents a human oesophageal cancer-associated antigen,
CC NY-ESO-1. The cDNA encoding this sequence was isolated from a cDNA
CC library prepared from a specimen of well-to-moderately differentiated
CC squamous cell cancer of the oesophagus. Expression analysis demonstrated
CC that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma
CC cell lines and in normal ovary and testis tissue, but not in normal
CC colon, kidney, liver or brain tissue. Analysis of the amino acid sequence
CC of the protein indicates that the protein has a transmembrane domain,
CC several N-myristoylation sites and O-phosphorylation sites and that it
CC contains antigenic sequences in the N-terminal half of the protein. The
CC antigen is useful as an immunogen when combined with an adjuvant, in both
CC precursor and post- translationally modified forms, and may be used to
CC generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic
CC marker for oesophageal cancer, and can be utilised as a marker for the
CC targetted delivery of therapeutic agents to oesophageal cancer cells. It
CC can also be used to generate diagnostic or therapeutic agents
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 68; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AARASGPGGGAPR 13
||||||||||||
Db 50 AARASGPGGGAPR 62

RESULT 13
AAB69946

ID AAB69946 standard; protein; 180 AA.
XX
AC AAB69946;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 protein.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX
CS Homo sapiens.
XX
PN WO200107917-A1.
XX
PD 01-FEB-2001.
XX
PF 14-JUL-2000; 2000WO-US019220.
XX
PR 23-JUL-1999; 99US-00359503.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX
DR WPI; 2001-182822/18.
DR N-PSDB; AAF58634.
XX
PT Method useful for determining the status (e.g. progression, regression or
PT stability of the disease) of a cancerous condition, involves determining
PT the levels of NY-ESO-1 specific antibodies in a sample taken from a
PT patient.
XX
PS Example 5; Fig 3; 50pp; English.
XX
CC The present sequence is human NY-ESO-1 protein. It is provided in a
CC specification relating to a method for determining the status of a
CC cancerous condition in a patient with a tumour that expresses NY-ESO-1.
CC The method comprises assaying a sample taken from the patient for
CC antibodies that specifically bind to the NY-ESO-1 and comparing the value
CC obtained to a prior value obtained from assay of a prior sample taken
CC from the patient. Any difference between the values is indicative of a
CC change in status of the cancerous condition. The method is useful for
CC determining whether a cancerous condition is progressing, regressing or
CC remaining stable, in particular in patients receiving treatment for a
CC melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
CC carcinoma
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 68; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AARASGPGGGAPR 13
||||||||||||
Db 50 AARASGPGGGAPR 62

RESULT 14
AAG67164
ID AAG67164 standard; protein; 180 AA.
XX
AC AAG67164;
XX
DT 13-NOV-2001 (first entry)
XX
DE Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
XX
KW Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
KW cancer; testis tumour.
XX
OS Homo sapiens.
XX
PN WO200162917-A1.
XX
PD 30-AUG-2001.
XX
PF 22-JAN-2001; 2001WO-US002126.
XX
PR 22-FEB-2000; 2000US-00510635.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Lethe B, Boon-Falleur T;
XX
DR WPI; 2001-550091/61.
DR N-PSDB; AAH75118.
XX
PT Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful
PT for diagnosing testicular tumors.
XX
PS Example 5; Fig 3; 50pp; English.
XX
CC The present sequence represents cancer testis tumour antigen NY-ESO-1
CC (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
CC least one human leukocyte antigen (HLA) binding peptide, which binds to
CC Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is
CC expressed in tumour mRNA and in testis, but not normal colon, kidney,
CC liver or brain tissue. The presence or level of expression of NY-ESO-1
CC may be assayed for the diagnosis of cancer, especially testis tumours
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 68; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AARASGPGGGAPR 13
||||||||||||
Db 50 AARASGPGGGAPR 62

RESULT 15
AAU01535
ID AAU01535 standard; protein; 180 AA.
XX
AC AAU01535;
XX
DT 18-JUL-2001 (first entry)
XX
DE Human NY-ESO-1 tumour rejection antigen precursor protein.
XX
KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 7
FT /note= "Myristoylated"
FT Modified-site 9
FT /note= "Myristoylated"
FT Modified-site 11
FT /note= "Phosphorylated"
FT Modified-site 98
FT /note= "Phosphorylated"
FT Modified-site 134
FT /note= "Phosphorylated"

FT Modified-site 138
FT /note= "Phosphorylated"
XX
PN WO200123560-A2.
XX
PD 05-APR-2001.
XX
PF 26-SEP-2000; 2000WO-US026411.
XX
PR 29-SEP-1999; 99US-00408036.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Tureci O, Sahin U, Pfreundschuh M;
XX
DR WPI; 2001-266156/27.
DR N-PSDB; AAS02254.
XX
PT Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid sequence
PT found in tumor rejection antigen precursor used for stimulating
PT proliferation of helper T cells.
XX
PS Claim 4; Fig 3; 62pp; English.
XX
CC The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to
CC major histocompatibility complex (MHC) Class II molecules such as human
CC leukocyte antigen-determining region (HLA-DR) molecules and stimulate
CC proliferation of helper T cells. The peptides can be administered to an
CC HLA-DR positive subject in order to stimulate the helper T cells. An MHC
CC Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell
CC or present in free form is useful for this stimulation. The nucleic acid
CC is useful for screening for a cancerous condition, which involves
CC contacting a subject sample to a cell line transfected with the
CC immunoreactive cell (helper T cell), where interaction is indicative of
CC cancer. In addition, a sample from a patient (for example, a body fluid
CC or tissue) can be monitored for the amount of the complex present in the
CC bloodstream. This is useful for determining regression, progression or
CC onset of a cancerous condition. The method involves contacting the sample
CC with a radioactive labelled or enzyme labelled monoclonal antibody which
CC specifically binds with the complex
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 68; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62
```

Search completed: March 13, 2006, 19:03:59
Job time : 97.8824 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:04:24 ; Search time 15.4471 Seconds
(without alignments)
80.975 Million cell updates/sec

Title: US-09-529-206E-28
Perfect score: 68
Sequence: 1 AARASGPGGGAPR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	44	64.7	82	2	T04476	acclimation protei
2	44	64.7	286	2	S04673	H+-transporting tw
3	44	64.7	379	1	A48082	MAP kinase 3 (EC 2
4	44	64.7	3190	2	T13828	CREB-binding prote
5	43	63.2	185	2	T36874	hypothetical prote
6	43	63.2	213	2	S42585	DNA-invertase - Rh
7	43	63.2	222	2	T36115	probable oxidoredu
8	43	63.2	349	2	S55626	hypothetical prote
9	43	63.2	377	2	S28184	Ca2+/calmodulin-de
10	43	63.2	380	2	JC1451	Ca2+/calmodulin-de
11	43	63.2	679	2	S02165	regulatory protein
12	43	63.2	954	2	A87431	regulatory protein
13	42	61.8	143	2	H87399	peptidyl-tRNA hydr
14	42	61.8	201	2	G72663	hypothetical prote
15	42	61.8	327	2	T29031	hypothetical prote
16	42	61.8	335	2	S08341	myristylated alani
17	42	61.8	351	2	S50754	hypothetical prote
18	42	61.8	378	2	C87425	aldose 1-epimerase
19	42	61.8	387	2	T52451	endopeptidase Clp
20	42	61.8	436	2	T36104	conserved hypothet
21	42	61.8	474	2	G75580	conserved hypothet
22	42	61.8	1690	2	T35694	ATP dependent DNA
23	41.5	61.0	521	2	A29345	steroid hormone re
24	41	60.3	134	2	AB2695	hypothetical prote
25	41	60.3	134	2	B97477	hypothetical prote
26	41	60.3	173	2	AB3648	flagellar basal-bo
27	41	60.3	357	2	F82878	XAA-PRO aminopepti
28	41	60.3	371	2	T39312	hypothetical prote
29	41	60.3	389	2	T15102	hypothetical prote
30	41	60.3	505	2	S68518	tub protein, brain
31	41	60.3	627	2	A44112	spidroin 2, dragli
32	41	60.3	1207	2	T00378	KIAA0641 protein -
33	40	58.8	190	1	JWEBT	DNA-invertase - Sa
34	40	58.8	290	2	T36712	hypothetical prote
35	40	58.8	291	1	S31415	glycine-rich prote
36	40	58.8	294	2	T17265	hypothetical prote
37	40	58.8	383	2	A86182	hypothetical prote
38	40	58.8	575	2	A47214	Jk-recombination s
39	40	58.8	910	2	A34721	androgen receptor
40	40	58.8	911	2	B34721	androgen receptor
41	40	58.8	919	2	A39248	androgen receptor
42	39.5	58.1	328	2	A44192	heterogeneous nucl
43	39.5	58.1	730	2	A36226	collagen alpha 1 c
44	39.5	58.1	3436	2	S55659	tegument protein 6
45	39	57.4	103	2	C72683	hypothetical prote

ALIGNMENTS

RESULT 1
T04476
acclimation protein 2 - barley
C;Species: Hordeum vulgare (barley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04476
R;Phillips, J.R.; Dunn, M.A.; Hughes, M.A.
Plant Mol. Biol. 33, 1013-1023, 1997
A;Title: mRNA stability and localisation of the low temperature responsive barley gene
A;Reference number: Z15367; MUID:97299834; PMID:9154983
A;Accession: T04476
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-82 <PHI>
A;Cross-references: UNIPROT:Q40033; UNIPARC:UPI000009CE5A; EMBL:X97917; NID:g1418969; P
A;Experimental source: cv. Igri
C;Genetics:
A;Gene: blt14.2

Query Match 64.7%; Score 44; DB 2; Length 82;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 AARASGPGGGAP 12
              ||| :| ||| |
Db         32 AARGAGAGGGVP 43
```

RESULT 2
S04673
H+-transporting two-sector ATPase (EC 3.6.3.14) gamma chain - Rhodopseudomonas blastica
C;Species: Rhodopseudomonas blastica
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 31-Dec-2004
C;Accession: S04673
R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A;Title: Rhodopseudomonas blastica atp operon. Nucleotide sequence and transcription.
A;Reference number: S04666; MUID:85058188; PMID:6209404
A;Accession: S04673
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-286 <TYB>
A;Cross-references: UNIPROT:P05436; UNIPARC:UPI0000126582
C;Superfamily: H(+)-transporting ATP synthase gamma chain
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

Query Match 64.7%; Score 44; DB 2; Length 286;
Best Local Similarity 69.2%; Pred. No. 40;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 AARASGPGGGAPR 13
              |: ||| | ||||
```

```
Db         54 ASLASGQGAGAPR 66


RESULT 3
A48082
MAP kinase 3 (EC 2.7.1.-) - human
N;Alternate names: extracellular signal-regulated kinase 1 (ERK1); mitogen-activated prc
N;Contains: protein kinase (EC 2.7.1.37)
C;Species: Homo sapiens (man)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C;Accession: A48082; PQ0270; S23428; S15519; S21579
R;Charest, D.L.; Mordret, G.; Harder, K.W.; Jirik, F.; Pelech, S.L.
Mol. Cell. Biol. 13, 4679-4690, 1993
A;Title: Molecular cloning, expression, and characterization of the human mitogen-activa
A;Reference number: A48082; MUID:93330262; PMID:7687743
A;Accession: A48082
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-379 <CHA>
A;Cross-references: UNIPROT:P27361; UNIPARC:UPI0000035BE2; EMBL:X60188; NID:g31220; PIDN
A;Experimental source: hepatoma cell line HEP G2
A;Note: authors translated the codon AGC for residue 174 as Ile
R;Owaki, H.; Makar, R.; Boulton, T.G.; Cobb, M.H.; Geppert, T.D.
Biochem. Biophys. Res. Commun. 182, 1416-1422, 1992
A;Title: Extracellular signal-regulated kinases in T cells: characterization of human ER
A;Reference number: JQ1400; MUID:92171961; PMID:1540184
A;Accession: PQ0270
A;Molecule type: mRNA
A;Residues: 14-173,'I',175-379 <OWA>
A;Cross-references: UNIPARC:UPI000016AB99; GB:M84490; NID:g186695; PIDN:AAA36142.1; PID:
A;Experimental source: cell line CEM
R;Gonzalez, F.A.; Raden, D.L.; Rigby, M.R.; Davis, R.J.
FEBS Lett. 304, 170-178, 1992
A;Title: Heterogeneous expression of four MAP kinase isoforms in human tissues.
A;Reference number: S23426; MUID:92316223; PMID:1319925
A;Accession: S23428
A;Molecule type: mRNA
A;Residues: 25-173,'I',175-379 <GON>
A;Cross-references: UNIPARC:UPI000016A2B4; EMBL:Z11696; NID:g23882; PIDN:CAA77754.1; PID
C;Comment: This enzyme is activated by MAP kinase kinase (see PIR:45100 and PIR:A46723).
C;Genetics:
A;Gene: GDB:PRKM3; ERK1
A;Cross-references: GDB:135679; OMIM:601795
A;Map position: 16pter-16qter
C;Complex: monomer
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Pathway: MAP kinase cascade
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; monomer; phosphoprotein; phosphotransferase; serine/threonine-specific
F;40-330/Domain: protein kinase homology <KIN>
F;48-56/Region: protein kinase ATP-binding motif
F;202/Binding site: phosphate (Thr) (covalent) (by MAP kinase kinase) #status predicted
F;204/Binding site: phosphate (Tyr) (covalent) (by MAP kinase kinase) #status predicted

  Query Match             64.7%;  Score 44;  DB 1;  Length 379;
  Best Local Similarity   69.2%;  Pred. No. 51;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              || | | ||| ||
Db          3 AAAAQGQGGGEPR 15


RESULT 4
T13828
CREB-binding protein homolog - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13828
R;Akimaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; Go
Nature 386, 735-738, 1997
A;Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling.
A;Reference number: Z17785; MUID:97263578; PMID:9109493
A;Accession: T13828
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3190 <AKI>
A;Cross-references: UNIPROT:O01368; UNIPARC:UPI000003EB83; EMBL:U88570; NID:g1916929; PI
C;Genetics:
A;Cross-references: FlyBase:FBgn0015624
A;Map position: X
F;1723-1780/Domain: bromodomain homology <BRO>

  Query Match             64.7%;  Score 44;  DB 2;  Length 3190;
  Best Local Similarity   77.8%;  Pred. No. 3.2e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 SGPGGGAPR 13
              :||||| ||
Db        320 NGPGGGGPR 328


RESULT 5
T36874
hypothetical protein SCI51.11c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36874
R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21617
A;Accession: T36874
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-185 <MUR>
A;Cross-references: UNIPROT:Q9S229; UNIPARC:UPI00000DB31A; EMBL:AL109848; PIDN:CAB52835
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCI51.11c

  Query Match             63.2%;  Score 43;  DB 2;  Length 185;
  Best Local Similarity   72.7%;  Pred. No. 38;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGA 11
              :|| |||| ||
Db         85 SARGSGPGSGA 95


RESULT 6
S42585
DNA-invertase - Rhizobium leguminosarum transposon Tn163
N;Alternate names: resolvase
C;Species: Rhizobium leguminosarum
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S42585
R;Ulrich, A.; Puehler, A.
Mol. Gen. Genet. 242, 505-516, 1994
A;Title: The new class II transposon Tn163 is plasmid-borne in two unrelated Rhizobium l
A;Reference number: S42584; MUID:94166763; PMID:8121409
A;Accession: S42585
A;Molecule type: DNA
A;Residues: 1-213 <ULR>
A;Cross-references: UNIPROT:Q52760; UNIPARC:UPI00000AE947; EMBL:L14931; NID:g349099; PID
A;Experimental source: strain E163N; class II transposon Tn163
C;Genetics:
A;Gene: tnpR
A;Genome: transposon Tn163
C;Superfamily: transposase repressor
C;Keywords: DNA binding; DNA integration; DNA recombination
F;11/Active site: Ser #status predicted

  Query Match             63.2%;  Score 43;  DB 2;  Length 213;
  Best Local Similarity   75.0%;  Pred. No. 42;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy          1 AARASGPGGGAP 12
              |||| |  ||||
Db        137 AARARGRNGGAP 148
```

RESULT 7
T36115
probable oxidoreductase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C;Accession: T36115
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1999
A;Reference number: Z21597
A;Accession: T36115
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-222 <MUR>
A;Cross-references: UNIPROT:Q9X887; UNIPARC:UPI00000DB008; EMBL:AL049707; PIDN:CAB41281.
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCE15.12c
C;Superfamily: NAD(P)H-dependent FMN reductase (sulfate starvation-induced protein 4); S

```
  Query Match           63.2%;  Score 43;  DB 2;  Length 222;
  Best Local Similarity   66.7%;  Pred. No. 44;
  Matches    8;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAP 12
              :||||||  | |
Db        182 SARASGPSAGRP 193
```

RESULT 8
S55626
hypothetical protein 32 - equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55626
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
A;Accession: S55626
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-349 <TEL>
A;Cross-references: UNIPROT:Q66635; UNIPARC:UPI00000EDFA7; GB:U20824; NID:g695172; PIDN:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995

```
  Query Match           63.2%;  Score 43;  DB 2;  Length 349;
  Best Local Similarity   69.2%;  Pred. No. 65;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              || ||||| |: |
Db         34 AAEASGPGPGSGR 46
```

RESULT 9
S28184
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) erk-1 - mouse (fragment)
N;Alternate names: extracellular signal-regulated kinase 1
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
C;Accession: S28184; B40466; A41371
R;Tanner, B.; Mueckler, M.
Biochim. Biophys. Acta 1171, 319-320, 1993
A;Title: Molecular cloning of a mouse extracellular signal regulated kinase (erk-1).
A;Reference number: S28184; MUID:93144347; PMID:8424957
A;Accession: S28184
A;Molecule type: mRNA
A;Residues: 1-377 <TAN>
A;Cross-references: UNIPROT:Q63844; UNIPARC:UPI000017558C; EMBL:Z14249
R;De Miguel, C.; Kligman, D.; Patel, J.; Detera-Wadleigh, S.D.
DNA Cell Biol. 10, 505-514, 1991
A;Title: Molecular analysis of microtubule-associated protein-2 kinase cDNA from mouse
A;Reference number: A40466; MUID:91369479; PMID:1716439
A;Accession: B40466
A;Molecule type: mRNA
A;Residues: 74-377 <DEM>
A;Cross-references: UNIPARC:UPI0000023599; GB:S59517
R;Crews, C.M.; Alessandrini, A.A.; Erikson, R.L.
Proc. Natl. Acad. Sci. U.S.A. 88, 8845-8849, 1991
A;Title: Mouse Erk-1 gene product is a serine/threonine protein kinase that has the pot
A;Reference number: A41371; MUID:92020947; PMID:1717989
A;Accession: A41371
A;Molecule type: mRNA
A;Residues: 7-16 <CRE>
A;Cross-references: UNIPARC:UPI0000170C57; GB:S58470; NID:g236372; PIDN:AAB19973.1; PID
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; calmodulin binding; phosphotransferase; protein kinase
F;38-328/Domain: protein kinase homology <KIN>
F;46-54/Region: protein kinase ATP-binding motif

```
  Query Match           63.2%;  Score 43;  DB 2;  Length 377;
  Best Local Similarity   69.2%;  Pred. No. 69;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              || | | ||| ||
Db          1 AAAAPGGGGGEPR 13
```

RESULT 10
JC1451
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) - rat
N;Alternate names: ERK1-MAP kinase; extracellular signal-regulated kinase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JC1451; A35061; A37140; A40466; S24947
R;Marquardt, B.; Stabel, S.
Gene 120, 297-299, 1992
A;Title: Sequence of a rat cDNA encoding the ERK1-MAP kinase.
A;Reference number: JC1451; MUID:93013050; PMID:1327976
A;Accession: JC1451
A;Molecule type: mRNA
A;Residues: 1-380 <MAR>
A;Cross-references: UNIPROT:P21708; UNIPARC:UPI000012F174; EMBL:X65198; NID:g56626; PID
A;Experimental source: brain
R;Boulton, T.G.; Yancopoulos, G.D.; Gregory, J.S.; Slaughter, C.; Moomaw, C.; Hsu, J.;
Science 249, 64-67, 1990
A;Title: An insulin-stimulated protein kinase similar to yeast kinases involved in cell
A;Reference number: A35061; MUID:90312137; PMID:2164259
A;Accession: A35061
A;Molecule type: mRNA
A;Residues: 14-380 <BOU>
A;Cross-references: UNIPARC:UPI0000145072; GB:M38194; NID:g204051; PIDN:AAA41123.1; PID
R;Boulton, T.G.; Gregory, J.S.; Cobb, M.H.
Biochemistry 30, 278-286, 1991
A;Title: Purification and properties of extracellular signal-regulated kinase 1, an insu
A;Reference number: A37140; MUID:91105092; PMID:1846291
A;Accession: A37140
A;Status: preliminary
A;Molecule type: protein
A;Residues: 43-64;167-178,'X',180-183,'X',185 <BO2>
A;Cross-references: UNIPARC:UPI000017558F; UNIPARC:UPI0000175590
R;De Miguel, C.; Kligman, D.; Patel, J.; Detera-Wadleigh, S.D.
DNA Cell Biol. 10, 505-514, 1991
A;Title: Molecular analysis of microtubule-associated protein-2 kinase cDNA from mouse
A;Reference number: A40466; MUID:91369479; PMID:1716439
A;Accession: A40466
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 14-94,'R',96-380 <DEM>
```
```

A;Cross-references: UNIPARC:UPI00001707CE; GB:U12008; GB:S59509; NID:g515498; PIDN:AAA20
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; calmodulin binding; phosphoprotein; phosphotransferase; serine/threonin
F;41-331/Domain: protein kinase homology <KIN>
F;49-57/Region: protein kinase ATP-binding motif

Query Match 63.2%; Score 43; DB 2; Length 380;
Best Local Similarity 69.2%; Pred. No. 70;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AARASGPGGGAPR 13
|| | | ||| ||
Db 4 AAAAPGGGGGEPR 16

RESULT 11
S02165
regulatory protein flaY - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S02165
R;Kaplan, J.B.; Dingwall, A.; Bryan, R.; Champer, R.; Shapiro, L.
J. Mol. Biol. 205, 71-83, 1989
A;Title: Temporal regulation and overlap organization of two Caulobacter flagellar genes
A;Reference number: S02164; MUID:89178645; PMID:2648000
A;Accession: S02165
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-679 <KAP>
A;Cross-references: UNIPROT:P15345; UNIPARC:UPI000017A8F7
C;Genetics:
A;Gene: flaY
C;Keywords: transcription regulation

Query Match 63.2%; Score 43; DB 2; Length 679;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AARASGPGGGAP 12
| | ||| |||
Db 170 AGTAGGPGAGAP 181

RESULT 12
A87431
regulatory protein FlaEY [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87431
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87431
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-954 <STO>
A;Cross-references: UNIPROT:P15345; UNIPARC:UPI000012A8ED; GB:AE005673; NID:g13422833; P
C;Genetics:
A;Gene: CC1465

Query Match 63.2%; Score 43; DB 2; Length 954;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AARASGPGGGAP 12
| | ||| |||
Db 314 AGTAGGPGAGAP 325

RESULT 13
H87399
peptidyl-tRNA hydrolase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: H87399
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: H87399
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-143 <STO>
A;Cross-references: UNIPROT:Q9A8Y3; UNIPARC:UPI00000C72F1; GB:AE005673; NID:g13422540; I
C;Genetics:
A;Gene: CC1214

Query Match 61.8%; Score 42; DB 2; Length 143;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AARASGPGG 9
| |||||||
Db 22 ATRASGPGG 30

RESULT 14
G72663
hypothetical protein APE0734 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72663
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takal
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: G72663
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-201 <KAW>
A;Cross-references: UNIPROT:Q9YE35; UNIPARC:UPI000005DC7C; DDBJ:AP000060; NID:g5104188;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0734
C;Superfamily: Aeropyrum pernix hypothetical protein APE0734

Query Match 61.8%; Score 42; DB 2; Length 201;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ARASGPGGGAPR 13
||||| || ||
Db 37 ARASGVGGRRPR 48

RESULT 15
T29031
hypothetical protein F53G12.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29031
R;Wu, X.; Graves, T.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F53G12.
A;Reference number: Z20555
A;Accession: T29031
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-327 <WUX>
A;Cross-references: UNIPROT:O01799; UNIPARC:UPI0000078FFF; EMBL:AF003139; PIDN:AAB54156

A;Experimental source: strain Bristol N2; clone F53G12
C;Genetics:
A;Gene: CESP:F53G12.7
A;Map position: 1
A;Introns: 59/3; 138/1; 223/2

Query Match 61.8%; Score 42; DB 2; Length 327;
Best Local Similarity 72.7%; Pred. No. 85;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 ARASGPGGGAP 12
              | |:| |||||
Db        113 AEAAGGGGGAP 123
```

Search completed: March 13, 2006, 19:16:11
Job time : 16.4471 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 18:53:23 ; Search time 94.3647 Seconds
(without alignments)
97.196 Million cell updates/sec

Title: US-09-529-206E-28
Perfect score: 68
Sequence: 1 AARASGPGGGAPR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	68	100.0	142	2	Q9NY13_HUMAN	Q9ny13 homo sapien
2	68	100.0	180	1	CTG1B_HUMAN	P78358 homo sapien
3	68	100.0	180	2	Q7LBY4_HUMAN	Q7lby4 homo sapien
4	60	88.2	210	1	CTAG2_HUMAN	O75638 homo sapien
5	54	79.4	362	2	Q63QT8_BURPS	Q63qt8 burkholderi
6	54	79.4	362	2	Q62H22_BURMA	Q62h22 burkholderi
7	52	76.5	321	2	Q96S27_HUMAN	Q96s27 homo sapien
8	51	75.0	367	2	Q6AV33_ORYSA	Q6av33 oryza sativ
9	50	73.5	194	2	Q96BU2_HUMAN	Q96bu2 homo sapien
10	50	73.5	895	2	Q4NUK4_9DELT	Q4nuk4 anaeromyxob
11	50	73.5	896	2	Q96D18_HUMAN	Q96d18 homo sapien
12	50	73.5	1253	2	Q6DHV6_HUMAN	Q6dhv6 homo sapien
13	50	73.5	1430	2	Q9H7P9_HUMAN	Q9h7p9 homo sapien
14	49	72.1	175	1	PACA_CHICK	P41534 g glucagon-
15	49	72.1	322	2	Q67PJ0_SYMTH	Q67pj0 symbiobacte
16	49	72.1	788	2	Q4QQP8_HUMAN	Q4qqp8 homo sapien
17	48	70.6	159	2	Q63KC9_BURPS	Q63kc9 burkholderi
18	48	70.6	159	2	Q62DA7_BURMA	Q62da7 burkholderi
19	48	70.6	262	2	Q5Z8E2_ORYSA	Q5z8e2 oryza sativ
20	48	70.6	449	2	Q7F1E3_ORYSA	Q7f1e3 oryza sativ
21	48	70.6	1133	2	Q4SDN7_TETNG	Q4sdn7 tetraodon n
22	48	70.6	3753	2	Q846W6_STRCM	Q846w6 streptomyce
23	47	69.1	108	2	Q8H321_ORYSA	Q8h321 oryza sativ
24	47	69.1	178	2	Q5AF08_CANAL	Q5af08 candida alb
25	47	69.1	702	2	Q4NQW2_9DELT	Q4nqw2 anaeromyxob
26	46	67.6	327	2	Q63HT9_BURPS	Q63ht9 burkholderi
27	46	67.6	330	2	Q629N3_BURMA	Q629n3 burkholderi
28	46	67.6	341	2	Q6H6A6_ORYSA	Q6h6a6 oryza sativ
29	46	67.6	359	2	Q6Z528_ORYSA	Q6z528 oryza sativ
30	46	67.6	383	2	Q4TEG9_TETNG	Q4teg9 tetraodon n
31	46	67.6	398	2	Q8N6H2_HUMAN	Q8n6h2 homo sapien
32	46	67.6	398	2	Q5SQU1_HUMAN	Q5squ1 homo sapien
33	46	67.6	399	2	Q8IVQ3_HUMAN	Q8ivq3 homo sapien
34	46	67.6	425	2	Q4NNI2_9DELT	Q4nni2 anaeromyxob
35	46	67.6	447	2	Q9GRA8_GRYBI	Q9gra8 gryllus bim
36	46	67.6	566	2	Q5SQT4_HUMAN	Q5sqt4 homo sapien
37	46	67.6	644	2	Q688J5_ORYSA	Q688j5 oryza sativ
38	46	67.6	684	2	Q51415_PSEAE	Q51415 pseudomonas
39	46	67.6	695	2	Q4T320_TETNG	Q4t320 tetraodon n
40	46	67.6	708	2	Q5KJM5_CRYNE	Q5kjm5 cryptococcu
41	46	67.6	708	2	Q55WM1_CRYNE	Q55wm1 cryptococcu
42	46	67.6	935	2	Q4P9H9_USTMA	Q4p9h9 ustilago ma
43	46	67.6	1000	2	Q4FKF7_9TRYP	Q4fkf7 trypanosoma
44	45	66.2	309	2	Q63N33_BURPS	Q63n33 burkholderi
45	45	66.2	310	2	Q89JY8_BRAJA	Q89jy8 bradyrhizob

ALIGNMENTS

RESULT 1
Q9NY13_HUMAN
ID Q9NY13_HUMAN PRELIMINARY; PRT; 142 AA.
AC Q9NY13;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein LAGE-2 (Fragment).
GN Name=LAGE-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ275978; CAB76945.1; -; mRNA.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;

Query Match 100.0%; Score 68; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         24 AARASGPGGGAPR 36
```

RESULT 2
CTG1B_HUMAN
ID CTG1B_HUMAN STANDARD; PRT; 180 AA.
AC P78358;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-
DE ESO-1).
GN Name=CTAG1B; Synonyms=CTAG, CTAG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
RA Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,
RA Williamson B., Stockert E., Pfreundschuh M., Old L.J.;
RT "A testicular antigen aberrantly expressed in human cancers detected
RT by autologous antibody screening.";

```
RL   Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Melanoma;
RX   MEDLINE=98289662; PubMed=9626360;
RA   Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA   de Plaen E., Boon T.;
RT   "LAGE-1, a new gene with tumor specificity.";
RL   Int. J. Cancer 76:903-908(1998).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98430682; PubMed=9759882;
RA   Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,
RA   Schwartzentruber D.J., Rosenberg S.A.;
RT   "A breast and melanoma-shared tumor antigen: T cell responses to
RT   antigenic peptides translated from different open reading frames.";
RL   J. Immunol. 161:3596-3606(1998).
CC   -!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide
CC       variety of cancers. Detected in uterine myometrium.
CC   -!- SIMILARITY: Belongs to the CTAG family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U87459; AAB49693.1; -; mRNA.
DR   EMBL; AJ003149; CAA05908.1; -; mRNA.
DR   EMBL; AF038567; AAD05202.1; -; mRNA.
DR   HGNC; HGNC:2491; CTAG1B.
DR   MIM; 300156; -.
KW   Antigen; Transmembrane.
FT   TRANSMEM    156    172       Potential.
FT   COMPBIAS      5     82       Gly-rich.
SQ   SEQUENCE   180 AA;  17992 MW;  B122C5C2C8BE1569 CRC64;

  Query Match             100.0%;  Score 68;  DB 1;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.071;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62


RESULT 3
Q7LBY4_HUMAN
ID   Q7LBY4_HUMAN PRELIMINARY;      PRT;   180 AA.
AC   Q7LBY4;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
DE   antigen 1-A).
GN   Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21303268;
RA   Galgoczy P., Rosenthal A., Platzer M.;
RT   "Human-mouse comparative sequence analysis of the NEMO gene reveals an
RT   alternative promoter within the neighboring G6PD gene.";
RL   Gene 271:93-98(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21566154; PubMed=11709543; DOI=10.1093/hmg/10.22.2557;
RA   Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
RA   Patlan H., Ciccodicola A., Kenwrick S., Platzer M., D'Urso M.,
RA   Nelson D.L.;
RT   "Multiple pathogenic and benign genomic rearrangements occur at a 35
RT   kb duplication involving the NEMO and LAGE2 genes.";
RL   Hum. Mol. Genet. 10:2557-2567(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Platzer M.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Platzer M.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RA   Galgoczy P., Platzer M.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99454989; PubMed=10523621;
RA   De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
RT   "DNA methylation is the primary silencing mechanism for a set of germ
RT   line- and tumor-specific genes with a CpG-rich promoter.";
RL   Mol. Cell. Biol. 19:7327-7335(1999).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RA   Lethe B.G.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF277315; AAL27014.1; -; Genomic_DNA.
DR   EMBL; AJ275977; CAB76943.1; -; Genomic_DNA.
DR   EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
SQ   SEQUENCE   180 AA;  17992 MW;  B122C5C2C8BE1569 CRC64;

  Query Match             100.0%;  Score 68;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.071;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62


RESULT 4
CTAG2_HUMAN
ID   CTAG2_HUMAN    STANDARD;      PRT;   210 AA.
AC   O75638; O75637; Q9BU80; Q9UJ89; Q9Y479;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
GN   Name=CTAG2; Synonyms=ESO2, LAGE1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B).
RC   TISSUE=Melanoma;
RX   MEDLINE=98289662; PubMed=9626360;
RA   Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA   de Plaen E., Boon T.;
RT   "LAGE-1, a new gene with tumor specificity.";
RL   Int. J. Cancer 76:903-908(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B), AND VARIANTS
RP   GLN-6; GLN-89 AND ARG-138.
RC   TISSUE=Melanoma;
RX   MEDLINE=99325550; PubMed=10399963;
RA   Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT   "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT   unexpected translation product of LAGE-1.";
RL   Int. J. Cancer 82:442-448(1999).
RN   [3]
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RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
RP   ARG-138.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=LAGE-1B; Synonyms=LAGE-1L;
CC         IsoId=O75638-1; Sequence=Displayed;
CC       Name=LAGE-1A; Synonyms=LAGE-1S;
CC         IsoId=O75638-2; Sequence=VSP_004301;
CC   -!- TISSUE SPECIFICITY: Testis and very low level in placenta and in
CC       some uterus samples. Observed in 25-50% of tumor samples of
CC       melanomas, non-small-cell lung carcinomas, bladder, prostate and
CC       head and neck cancers.
CC   -!- DOMAIN: A transmembrane domain is present in isoform LAGE-1A.
CC   -!- SIMILARITY: Belongs to the CTAG family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AJ223093; CAA11117.1; -; Genomic_DNA.
DR   EMBL; AJ223093; CAA11116.1; -; Genomic_DNA.
DR   EMBL; AJ223040; CAA11043.1; -; mRNA.
DR   EMBL; AJ223041; CAA11044.1; -; mRNA.
DR   EMBL; AJ012834; CAA10194.1; -; mRNA.
DR   EMBL; AJ012835; CAA10196.1; -; mRNA.
DR   EMBL; BC002833; AAH02833.1; -; mRNA.
DR   Ensembl; ENSG00000126890; Homo sapiens.
DR   HGNC; HGNC:2492; CTAG2.
DR   H-InvDB; HIX0017163; -.
DR   MIM; 300396; -.
KW   Alternative splicing; Antigen; Polymorphism; Transmembrane.
FT   COMPBIAS      5     79       Gly-rich.
FT   COMPBIAS    183    188       Poly-Pro.
FT   VARSPLIC    135    210       MSVWDQDREGAGRMRVVGWGLGSASPEGQKARDLRTPKHKV
FT                                SEQRPGTPGPPPPEGAQGDGCRGVAFNVMFSAPHI -> IR
FT                                LTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQAPSG
FT                                QRR (in isoform LAGE-1A).
FT                                /FTId=VSP_004301.
FT   VARIANT       6      6       R -> Q.
FT                                /FTId=VAR_007855.
FT   VARIANT      89     89       E -> Q.
FT                                /FTId=VAR_007856.
FT   VARIANT     138    138       W -> R.
FT                                /FTId=VAR_007857.
SQ   SEQUENCE   210 AA;  21120 MW;  8BE0EE00AE55E8BE CRC64;

  Query Match          88.2%;  Score 60;  DB 1;  Length 210;
  Best Local Similarity   92.3%;  Pred. No. 1.1;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              ||||||| |||||
Db         50 AARASGPRGGAPR 62


RESULT 5
Q63QT8_BURPS
ID   Q63QT8_BURPS PRELIMINARY;      PRT;   362 AA.
AC   Q63QT8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative DNA polymerase III.
GN   OrderedLocusNames=BPSL2936;
OS   Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia; pseudomallei group.
OX   NCBI_TaxID=28450;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=K96243;
RX   PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA   Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
RA   Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA   Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
RA   Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA   Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D.,
RA   Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA   Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA   Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA   Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA   Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT   "Genomic plasticity of the causative agent of melioidosis,
RT   Burkholderia pseudomallei.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR   EMBL; BX571965; CAH36946.1; -; Genomic_DNA.
DR   GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR   GO; GO:0006260; P:DNA replication; IEA.
DR   InterPro; IPR010372; DNA_pol3_delta.
DR   InterPro; IPR005790; DNA_polIII_delta.
DR   Pfam; PF06144; DNA_pol3_delta; 1.
DR   TIGRFAMs; TIGR01128; holA; 1.
KW   Complete proteome.
SQ   SEQUENCE   362 AA;  38726 MW;  D5FF3DE783D41E41 CRC64;

  Query Match          79.4%;  Score 54;  DB 2;  Length 362;
  Best Local Similarity   83.3%;  Pred. No. 13;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ARASGPGGGAPR 13
              |||:|||| |||
Db        348 ARAAGPGGDAPR 359


RESULT 6
Q62H22_BURMA
ID   Q62H22_BURMA PRELIMINARY;      PRT;   362 AA.
AC   Q62H22;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   DNA polymerase III, delta subunit (EC 2.7.7.7).
GN   Name=holA; OrderedLocusNames=BMA2451;
OS   Burkholderia mallei (Pseudomonas mallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia.
OX   NCBI_TaxID=13373;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ATCC 23344;
RX   PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA   Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
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RA   Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA   Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA   Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA   Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
RA   Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA   Zafar N., Zhou L., Fraser C.M.;
RT   "Structural flexibility in the Burkholderia mallei genome.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR   EMBL; CP000010; AAU49707.1; -; Genomic_DNA.
DR   TIGR; BMA2451; -.
DR   GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006260; P:DNA replication; IEA.
DR   InterPro; IPR010372; DNA_pol3_delta.
DR   InterPro; IPR005790; DNA_polIII_delta.
DR   Pfam; PF06144; DNA_pol3_delta; 1.
DR   TIGRFAMs; TIGR01128; holA; 1.
KW   Complete proteome; Nucleotidyltransferase; Transferase.
SQ   SEQUENCE   362 AA;  38726 MW;  D5FF3DE783D41E41 CRC64;

  Query Match             79.4%;  Score 54;  DB 2;  Length 362;
  Best Local Similarity   83.3%;  Pred. No. 13;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ARASGPGGGAPR 13
              |||:|||| |||
Db        348 ARAAGPGGDAPR 359


RESULT 7
Q96S27_HUMAN
ID   Q96S27_HUMAN PRELIMINARY;      PRT;   321 AA.
AC   Q96S27;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein gene X.
GN   Name=gene X;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21096910; PubMed=11157797; DOI=10.1093/hmg/10.4.339;
RA   Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA   Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA   Higgs D.R.;
RT   "Sequence, structure and pathology of the fully annotated terminal 2
RT   Mb of the short arm of human chromosome 16.";
RL   Hum. Mol. Genet. 10:339-352(2001).
DR   EMBL; AE006463; AAK61225.1; -; Genomic_DNA.
DR   Ensembl; ENSG00000167933; Homo sapiens.
KW   Hypothetical protein.
SQ   SEQUENCE   321 AA;  32979 MW;  9C8764CFA17F4CD4 CRC64;

  Query Match             76.5%;  Score 52;  DB 2;  Length 321;
  Best Local Similarity   76.9%;  Pred. No. 22;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              ||| :|||||| |
Db          5 AARRAGPGGGAAR 17


RESULT 8
Q6AV33_ORYSA
ID   Q6AV33_ORYSA PRELIMINARY;      PRT;   367 AA.
AC   Q6AV33;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein OSJNBa0063J18.9.
GN   Name=OSJNBa0063J18.9;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA   Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA   Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA   Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA   Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA   White O., Salzberg S.L., Fraser C.M.;
RT   "Oryza sativa chromosome 3 BAC OSJNBa0063J18 genomic sequence.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell R.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC107206; AAT77052.1; -; Genomic_DNA.
DR   Gramene; Q6AV33; -.
KW   Hypothetical protein.
SQ   SEQUENCE   367 AA;  37474 MW;  B8C62D9D4CC18C86 CRC64;

  Query Match             75.0%;  Score 51;  DB 2;  Length 367;
  Best Local Similarity   76.9%;  Pred. No. 35;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              || |||||||: |
Db         91 AAAASGPGGGSAR 103


RESULT 9
Q96BU2_HUMAN
ID   Q96BU2_HUMAN PRELIMINARY;      PRT;   194 AA.
AC   Q96BU2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   PLEKHG2 protein (Fragment).
GN   Name=PLEKHG2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pancreas;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pancreas;
RA   Director MGC Project;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC015174; AAH15174.1; -; mRNA.
FT   NON_TER       1       1
SQ   SEQUENCE   194 AA;  19957 MW;  91AB4FF8F05CBD3C CRC64;

  Query Match             73.5%;  Score 50;  DB 2;  Length 194;
  Best Local Similarity   81.8%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 ARASGPGGGAP 12
              ||  ||||||
Db         99 ARRQGPGGGAP 109


RESULT 10
Q4NUK4_9DELT
ID   Q4NUK4_9DELT PRELIMINARY;      PRT;   895 AA.
AC   Q4NUK4;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   LigA.
GN   ORFNames=AdehDRAFT_2813;
OS   Anaeromyxobacter dehalogenans 2CP-C.
OC   Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC   Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
OX   NCBI_TaxID=290397;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=2CP-C;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome assembly of Anaeromyxobacter
RT   dehalogenans 2CP-C.";
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=2CP-C;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Anaeromyxobacter
RT   dehalogenans 2CP-C.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAHD01000013; EAL79351.1; -; Genomic_DNA.
SQ   SEQUENCE   895 AA;  93871 MW;  0AE25BBBF172BDB0 CRC64;

  Query Match             73.5%;  Score 50;  DB 2;  Length 895;
  Best Local Similarity   76.9%;  Pred. No. 1.1e+02;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              | || | ||||||
Db        797 ARRARGAGGGAPR 809


RESULT 11
Q96D18_HUMAN
ID   Q96D18_HUMAN PRELIMINARY;      PRT;   896 AA.
AC   Q96D18;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PLEKHG2 protein.
GN   Name=PLEKHG2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pancreas;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pancreas;
RA   Director MGC Project;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013426; AAH13426.1; -; mRNA.
SQ   SEQUENCE   896 AA;  94247 MW;  0DE6869BCFD4C471 CRC64;

  Query Match             73.5%;  Score 50;  DB 2;  Length 896;
  Best Local Similarity   81.8%;  Pred. No. 1.1e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 ARASGPGGGAP 12
              ||  |||||||
Db        801 ARRQGPGGGAP 811


RESULT 12
Q6DHV6_HUMAN
ID   Q6DHV6_HUMAN PRELIMINARY;      PRT;  1253 AA.
AC   Q6DHV6;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   PLEKHG2 protein (Fragment).
GN   Name=PLEKHG2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pancreas;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pancreas;
RA   Director MGC Project;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 PH domain.
DR   EMBL; BC075858; AAH75858.1; -; mRNA.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR000219; RhoGEF.
DR   Pfam; PF00169; PH; 1.
DR   Pfam; PF00621; RhoGEF; 1.
DR   SMART; SM00233; PH; 1.
DR   SMART; SM00325; RhoGEF; 1.
DR   PROSITE; PS50010; DH_2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   1253 AA;  134404 MW;  534EB31283E535C5 CRC64;

  Query Match             73.5%;  Score 50;  DB 2;  Length 1253;
  Best Local Similarity   81.8%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 ARASGPGGGAP 12
              ||  |||||||
Db       1158 ARRQGPGGGAP 1168
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RESULT 13
Q9H7P9_HUMAN
ID   Q9H7P9_HUMAN PRELIMINARY;      PRT;  1430 AA.
AC   Q9H7P9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   FLJ00018 protein (Fragment).
GN   Name=PLEKHG2; Synonyms=FLJ00018;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   PubMed=14702039; DOI=10.1038/ng1285;
RA   Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA   Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA   Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA   Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA   Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA   Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA   Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA   Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA   Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA   Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA   Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA   Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA   Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA   Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA   Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA   Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA   Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA   Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA   Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
CC   -!- SIMILARITY: Contains 1 PH domain.
DR   EMBL; AK024429; BAB15719.1; -; mRNA.
DR   HSSP; Q64096; 1KZ7.
DR   Ensembl; ENSG00000090924; Homo sapiens.
DR   HGNC; HGNC:29515; PLEKHG2.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR000219; RhoGEF.
DR   Pfam; PF00169; PH; 1.
DR   Pfam; PF00621; RhoGEF; 1.
DR   SMART; SM00233; PH; 1.
DR   SMART; SM00325; RhoGEF; 1.
DR   PROSITE; PS50010; DH_2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   1430 AA;  152528 MW;  E4DF0BFDACCB6A30 CRC64;

  Query Match             73.5%;  Score 50;  DB 2;  Length 1430;
  Best Local Similarity   81.8%;  Pred. No. 1.7e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 ARASGPGGGAP 12
              ||  |||||||
Db       1335 ARRQGPGGGAP 1345
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RESULT 14
PACA_CHICK
ID   PACA_CHICK     STANDARD;      PRT;   175 AA.
AC   P41534; Q53WW0;
DT   01-NOV-1995 (Rel. 32, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Glucagon-family neuropeptides precursor [Contains: Growth hormone-
DE   releasing factor 1-46 (GRF) (Growth hormone-releasing hormone) (GHRH);
DE   Pituitary adenylate cyclase activating polypeptide-27 (PACAP-27)
DE   (PACAP27); Pituitary adenylate cyclase activating polypeptide-38
DE   (PACAP-38) (PACAP38)].
GN   Name=ADCYAP1;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].
RX   MEDLINE=97174314; PubMed=9022048;
RA   McRory J.E., Parker R.L., Sherwood N.M.;
RT   "Expression and alternative processing of a chicken gene encoding both
RT   growth hormone-releasing hormone and pituitary adenylate cyclase-
RT   activating polypeptide.";
RL   DNA Cell Biol. 16:95-102(1997).
RN   [2]
RP   PROTEIN SEQUENCE OF 131-168.
RA   Yasuhara T., Mizuno K., Somogyvari-Vigh A., Komaki G., Arimura A.;
RT   "Isolation and primary structure of chicken PACAP.";
RL   Regul. Pept. 37:326-326(1992).
CC   -!- FUNCTION: Primary role of GRF is to release GH from the pituitary.
CC   -!- FUNCTION: PACAP plays pivotal roles as a neurotransmitter and/or a
CC       neuromodulator.
CC   -!- SUBCELLULAR LOCATION: Secreted.
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CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=GRF 1-46;
CC         IsoId=P41534-1; Sequence=Displayed;
CC       Name=GRF 1-43;
CC         IsoId=P41534-2; Sequence=VSP_001760;
CC       Name=GRF 33-46;
CC         IsoId=P41534-3; Sequence=VSP_001759;
CC   -!- SIMILARITY: Belongs to the glucagon family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U71183; AAB51200.1; -; mRNA.
DR   EMBL; U71184; AAB51201.1; -; mRNA.
DR   EMBL; U71185; AAB51202.1; -; mRNA.
DR   EMBL; U67275; AAC64494.1; -; Genomic_DNA.
DR   HSSP; P18509; 1GEA.
DR   InterPro; IPR000532; Glucagon.
DR   Pfam; PF00123; Hormone_2; 2.
DR   PRINTS; PR00275; GLUCAGON.
DR   PROSITE; PS00260; GLUCAGON; 2.
KW   Alternative splicing; Amidation; Cleavage on pair of basic residues;
KW   Direct protein sequencing; Glucagon family; Hormone; Signal.
FT   SIGNAL       1     23       Potential.
FT   PROPEP      24     80
FT   PEPTIDE      83    128       Growth hormone-releasing factor 1-46.
FT   PEPTIDE     131    168       Pituitary adenylate cyclase activating
FT                                polypeptide-38.
FT   PEPTIDE     131    157       Pituitary adenylate cyclase activating
FT                                polypeptide-27.
FT   PROPEP      172    175
FT   MOD_RES     157    157       Leucine amide (G-158 provides amide
FT                                group).
FT   MOD_RES     168    168       Lysine amide (G-169 provides amide
FT                                group).
FT   VARSPLIC     82    114       RHADGIFSKAYRKLLGQLSARNYLHSLMAKRVG -> S
FT                                (in isoform GRF 33-46).
FT                                /FTId=VSP_001759.
FT   VARSPLIC    115    117       Missing (in isoform GRF 1-43).
FT                                /FTId=VSP_001760.
SQ   SEQUENCE   175 AA;  19561 MW;  0DB54995F0AA9DFB CRC64;

  Query Match             72.1%;  Score 49;  DB 1;  Length 175;
  Best Local Similarity   69.2%;  Pred. No. 33;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              | ||  |||| ||
Db         54 ALRAGAPGGGGPR 66


RESULT 15
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ID   Q67PJ0_SYMTH PRELIMINARY;      PRT;   322 AA.
AC   Q67PJ0;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Prephenate dehydrogenase.
GN   OrderedLocusNames=STH1418;
OS   Symbiobacterium thermophilum.
OC   Bacteria; Actinobacteria; Symbiobacterium.
OX   NCBI_TaxID=2734;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=IAM14863;
RX   PubMed=15383646; DOI=10.1093/nar/gkh830;
RA   Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
RA   Morimura K., Ikeda H., Hattori M., Beppu T.;
RT   "Genome sequence of Symbiobacterium thermophilum, an uncultivable
RT   bacterium that depends on microbial commensalism.";
RL   Nucleic Acids Res. 32:4937-4944(2004).
DR   EMBL; AP006840; BAD40403.1; -; Genomic_DNA.
DR   GO; GO:0004665; F:prephenate dehydrogenase (NADP+) activity; IEA.
DR   GO; GO:0006571; P:tyrosine biosynthesis; IEA.
DR   InterPro; IPR003099; Prephen_dehydrog.
DR   Pfam; PF02153; PDH; 1.
KW   Complete proteome.
SQ   SEQUENCE   322 AA;  32843 MW;  09A06AC0AFA734EC CRC64;

  Query Match             72.1%;  Score 49;  DB 2;  Length 322;
  Best Local Similarity   90.9%;  Pred. No. 58;
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Qy          1 AARASGPGGGA 11
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Db         45 AADASGPGGGA 55


Search completed: March 13, 2006, 19:14:27
Job time : 94.3647 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:14:49 ; Search time 24.1647 Seconds
(without alignments)
44.477 Million cell updates/sec

Title: US-09-529-206E-28
Perfect score: 68
Sequence: 1 AARASGPGGGAPR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	68	100.0	180	1	US-08-791-495-9	Sequence 9, Appli
2	68	100.0	180	2	US-08-937-263B-8	Sequence 8, Appli
3	68	100.0	180	2	US-09-751-798-8	Sequence 8, Appli
4	68	100.0	180	2	US-09-392-714-25	Sequence 25, Appl
5	68	100.0	180	2	US-09-165-546D-15	Sequence 15, Appl
6	68	100.0	180	2	US-09-341-829A-9	Sequence 9, Appli
7	68	100.0	180	2	US-09-849-602-30	Sequence 30, Appl
8	60	88.2	180	1	US-08-791-495-7	Sequence 7, Appli
9	60	88.2	180	2	US-09-341-829A-7	Sequence 7, Appli
10	60	88.2	210	1	US-08-791-495-5	Sequence 5, Appli
11	60	88.2	210	2	US-09-341-829A-5	Sequence 5, Appli
12	50	73.5	160	2	US-09-252-991A-17249	Sequence 17249, A
13	49	72.1	143	2	US-08-789-329C-10	Sequence 10, Appl
14	49	72.1	172	2	US-08-789-329C-7	Sequence 7, Appli
15	49	72.1	175	2	US-08-789-329C-3	Sequence 3, Appli
16	49	72.1	416	2	US-09-252-991A-30219	Sequence 30219, A
17	48	70.6	9	2	US-09-344-040C-117	Sequence 117, App
18	48	70.6	9	2	US-09-833-039A-117	Sequence 117, App
19	48	70.6	196	2	US-09-252-991A-30527	Sequence 30527, A
20	48	70.6	421	2	US-09-252-991A-32326	Sequence 32326, A
21	48	70.6	456	2	US-09-252-991A-17335	Sequence 17335, A
22	48	70.6	809	2	US-09-252-991A-31759	Sequence 31759, A
23	48	70.6	1427	2	US-09-252-991A-20577	Sequence 20577, A
24	46	67.6	210	2	US-09-252-991A-24923	Sequence 24923, A
25	46	67.6	789	2	US-09-252-991A-25611	Sequence 25611, A
26	45	66.2	187	2	US-09-252-991A-29442	Sequence 29442, A
27	45	66.2	678	2	US-10-104-047-3295	Sequence 3295, Ap
28	45	66.2	679	2	US-09-252-991A-27111	Sequence 27111, A
29	45	66.2	727	2	US-09-902-540-12383	Sequence 12383, A
30	44	64.7	186	2	US-09-252-991A-16943	Sequence 16943, A
31	44	64.7	242	2	US-08-220-602B-23	Sequence 23, Appl
32	44	64.7	242	2	US-09-861-012A-23	Sequence 23, Appl
33	44	64.7	242	2	US-09-861-098A-23	Sequence 23, Appl
34	44	64.7	242	2	US-09-861-097-23	Sequence 23, Appl
35	44	64.7	357	2	US-09-252-991A-28380	Sequence 28380, A
36	44	64.7	379	2	US-08-622-277A-8	Sequence 8, Appli
37	44	64.7	379	2	US-09-025-580-25	Sequence 25, Appl
38	44	64.7	379	2	US-09-411-628-14	Sequence 14, Appl
39	44	64.7	379	2	US-10-174-794-14	Sequence 14, Appl
40	44	64.7	379	2	US-09-538-092-1021	Sequence 1021, Ap
41	44	64.7	379	2	US-09-642-749-25	Sequence 25, Appl
42	44	64.7	631	2	US-09-417-197-39	Sequence 39, Appl
43	44	64.7	974	2	US-08-938-291A-4	Sequence 4, Appli
44	44	64.7	974	2	US-09-589-619-4	Sequence 4, Appli
45	43	63.2	165	2	US-09-270-767-59895	Sequence 59895, A

ALIGNMENTS

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RESULT 1
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL-1 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-791-495-9

  Query Match             100.0%;  Score 68;  DB 1;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.068;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
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Db         50 AARASGPGGGAPR 62
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RESULT 2
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
;  GENERAL INFORMATION:
;    APPLICANT:  Chen, Yao-Tseng; Scanlan, Matthew;
;    APPLICANT:  Gure, Ali; Old, Lloyd J.; Jager, Elke;
;    APPLICANT:  Alexander, Knuth; Drijfhout, Jan W.
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULE
;    TITLE OF INVENTION:  ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
;    TITLE OF INVENTION:  ITSELF, AND USES THEREOF
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/937,263B
;      FILING DATE:  September 15, 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sinn, Eric, Patent Agent
;      REGISTRATION NUMBER:  40,177
;      REFERENCE/DOCKET NUMBER:  LUD 5466.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3000
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-937-263B-8

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  Best Local Similarity   100.0%;  Pred. No. 0.068;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62


RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
;  GENERAL INFORMATION:
;    APPLICANT:  Stockert, Elisabeth; Jager, Elke;
;    APPLICANT:  Chen, Yao-tseng; Scanlan, Matthew;
;    APPLICANT:  Knuth, Alexander; Old, Lloyd J.
;    TITLE OF INVENTION:  Antibodies Which Bind to NY-ESO-1 Cancer
;    TITLE OF INVENTION:  Associated Proteins, Uses Thereof,
;    TITLE OF INVENTION:  Truncated Forms of NY-ESO-1, and HLA
;    TITLE OF INVENTION:  Binding Peptides Derived Therefrom
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/751,798
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/062,422
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 6525177man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3168
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-09-751-798-8

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  Best Local Similarity   100.0%;  Pred. No. 0.068;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62


RESULT 4
US-09-392-714-25
; Sequence 25, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT: Gure, Ali O.
;  APPLICANT: Williamson, Barbara
;  APPLICANT: Chen, Yao-Tseng
;  APPLICANT: Old, Lloyd J.
;  TITLE OF INVENTION: Cancer Associated Antigens and Uses
;  TITLE OF INVENTION: Therefor
;  FILE REFERENCE: L0461/7062
;  CURRENT APPLICATION NUMBER: US/09/392,714A
;  CURRENT FILING DATE: 1999-09-09
;  EARLIER APPLICATION NUMBER: PCT/US98/14679
;  EARLIER FILING DATE: 1998-07-15
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-392-714-25

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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
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Db         50 AARASGPGGGAPR 62
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RESULT 5
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; Sequence 15, Application US/09165546D
; Patent No. 6723832
;   GENERAL INFORMATION:
;        APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
;                   Gure, Ali, Old, Lloyd, Ritter, Gerd
;        TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                            SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
;                            USES THEREOF
;        NUMBER OF SEQUENCES: 15
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FULBRIGHT & JAWORSKI LLP
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10158
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/165,546D
;             FILING DATE: 02-Oct-1998
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: April 17, 1998
;             APPLICATION NUMBER: 08/937,263
;             FILING DATE: September 15, 1997
;             APPLICATION NUMBER: US 08/725,182
;             FILING DATE: October 3, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, No. 6723832man D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3000
;             TELEFAX: (212) 318-3400
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 180 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15

  Query Match             100.0%;  Score 68;  DB 2;  Length 180;
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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62


RESULT 6
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-9

  Query Match             100.0%;  Score 68;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.068;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62


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US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT:  Old, Lloyd J.
;  APPLICANT:  Stockert, Elisabeth
;  APPLICANT:  Chen, Yao-Tseng
;  TITLE OF INVENTION: Colon Cancer Antigen Panel
;  FILE REFERENCE: L0461/7105(JRV)
;  CURRENT APPLICATION NUMBER: US/09/849,602
;  CURRENT FILING DATE:  2001-05-04
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-849-602-30

  Query Match             100.0%;  Score 68;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.068;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
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Db         50 AARASGPGGGAPR 62


RESULT 8
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL-1 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-791-495-7

  Query Match             88.2%;  Score 60;  DB 1;  Length 180;
  Best Local Similarity   92.3%;  Pred. No. 0.75;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
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Db         50 AARASGPRGGAPR 62


RESULT 9
US-09-341-829A-7
; Sequence 7, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-7

  Query Match             88.2%;  Score 60;  DB 2;  Length 180;
  Best Local Similarity   92.3%;  Pred. No. 0.75;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              ||||||| |||||
Db         50 AARASGPRGGAPR 62


RESULT 10
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL-1 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  210 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-791-495-5

  Query Match             88.2%;  Score 60;  DB 1;  Length 210;
  Best Local Similarity   92.3%;  Pred. No. 0.86;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              ||||||| |||||
Db         50 AARASGPRGGAPR 62


RESULT 11
US-09-341-829A-5
; Sequence 5, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-5

  Query Match             88.2%;  Score 60;  DB 2;  Length 210;
  Best Local Similarity   92.3%;  Pred. No. 0.86;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              ||||||| |||||
Db         50 AARASGPRGGAPR 62


RESULT 12
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US-09-252-991A-17249
; Sequence 17249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17249
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17249

Query Match 73.5%; Score 50; DB 2; Length 160;
Best Local Similarity 69.2%; Pred. No. 13;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AARASGPGGGAPR 13
| | :|||| |||
Db 117 AGRRAGPGGSAPR 129

RESULT 13
US-08-789-329C-10
; Sequence 10, Application US/08789329C
; Patent No. 6165755
; GENERAL INFORMATION:
; APPLICANT: SHERWOOD ET AL.
; TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL
; TITLE OF INVENTION: FOR IMPROVED POULTRY PRODUCTION
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204-2988
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: WordPerfect 7.0 & ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,329C
; FILING DATE: 01/23/97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Earp, David J.
; REGISTRATION NUMBER: 41,401
; REFERENCE/DOCKET NUMBER: 2847-46468/DJE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 aa
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-789-329C-10

Query Match 72.1%; Score 49; DB 2; Length 143;
Best Local Similarity 69.2%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AARASGPGGGAPR 13
| || |||| ||
Db 54 ALRAGAPGGGGPR 66

RESULT 14
US-08-789-329C-7
; Sequence 7, Application US/08789329C
; Patent No. 6165755
; GENERAL INFORMATION:
; APPLICANT: SHERWOOD ET AL.
; TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL
; TITLE OF INVENTION: FOR IMPROVED POULTRY PRODUCTION
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204-2988
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: WordPerfect 7.0 & ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,329C
; FILING DATE: 01/23/97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Earp, David J.
; REGISTRATION NUMBER: 41,401
; REFERENCE/DOCKET NUMBER: 2847-46468/DJE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 172 aa
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-789-329C-7

Query Match 72.1%; Score 49; DB 2; Length 172;
Best Local Similarity 69.2%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AARASGPGGGAPR 13
| || |||| ||
Db 54 ALRAGAPGGGGPR 66

RESULT 15
US-08-789-329C-3
; Sequence 3, Application US/08789329C
; Patent No. 6165755
; GENERAL INFORMATION:
; APPLICANT: SHERWOOD ET AL.

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;    TITLE OF INVENTION:  CHICKEN NEUROPEPTIDE GENE USEFUL
;    TITLE OF INVENTION:  FOR IMPROVED POULTRY PRODUCTION
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klarquist Sparkman Campbell Leigh &
;      ADDRESSEE:  Whinston, LLP
;      STREET:  One World Trade Center
;      STREET:  121 S.W. Salmon Street
;      STREET:  Suite 1600
;      CITY:  Portland
;      STATE:  Oregon
;      COUNTRY:  United States of America
;      ZIP:  97204-2988
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Disk, 3-1/2 inch
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows NT
;      SOFTWARE:  WordPerfect 7.0 & ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/789,329C
;      FILING DATE:  01/23/97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Earp, David J.
;      REGISTRATION NUMBER:  41,401
;      REFERENCE/DOCKET NUMBER:  2847-46468/DJE
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (503) 226-7391
;      TELEFAX:  (503) 228-9446
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  175 aa
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-789-329C-3

  Query Match             72.1%;  Score 49;  DB 2;  Length 175;
  Best Local Similarity   69.2%;  Pred. No. 19;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              | ||  |||| ||
Db         54 ALRAGAPGGGGPR 66


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Job time : 24.1647 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:51:56 ; Search time 78.6118 Seconds
(without alignments)
69.096 Million cell updates/sec

Title: US-09-529-206E-28
Perfect score: 68
Sequence: 1 AARASGPGGGAPR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	68	100.0	30	4	US-10-296-734-1404	Sequence 1404, Ap
2	68	100.0	179	5	US-10-482-029-202	Sequence 202, App
3	68	100.0	180	3	US-09-751-798-8	Sequence 8, Appli
4	68	100.0	180	3	US-09-849-602-30	Sequence 30, Appl
5	68	100.0	180	4	US-10-023-182-8	Sequence 8, Appli
6	68	100.0	180	4	US-10-207-655-71	Sequence 71, Appl
7	68	100.0	180	4	US-10-364-614-14	Sequence 14, Appl
8	68	100.0	180	4	US-10-026-066-3	Sequence 3, Appli
9	68	100.0	180	4	US-10-117-937-74	Sequence 74, Appl
10	68	100.0	180	4	US-10-295-027-386	Sequence 386, App
11	68	100.0	180	4	US-10-296-734-832	Sequence 832, App
12	68	100.0	180	4	US-10-188-832-139	Sequence 139, App
13	68	100.0	180	4	US-10-777-053-11	Sequence 11, Appl
14	68	100.0	180	4	US-10-751-088-15	Sequence 15, Appl
15	68	100.0	180	4	US-10-657-022-74	Sequence 74, Appl
16	68	100.0	180	4	US-10-837-217-11	Sequence 11, Appl
17	68	100.0	180	5	US-10-877-373-9	Sequence 9, Appli
18	68	100.0	180	5	US-10-723-860-1270	Sequence 1270, Ap
19	68	100.0	180	5	US-10-871-708-7	Sequence 7, Appli
20	68	100.0	180	5	US-10-895-523-3	Sequence 3, Appli
21	68	100.0	180	5	US-10-182-506A-3	Sequence 3, Appli
22	68	100.0	180	5	US-10-756-149-5024	Sequence 5024, Ap
23	68	100.0	180	6	US-11-067-064-74	Sequence 74, Appl
24	68	100.0	180	6	US-11-067-159-74	Sequence 74, Appl
25	68	100.0	397	3	US-09-821-883-27	Sequence 27, Appl
26	68	100.0	397	6	US-11-144-912-27	Sequence 27, Appl
27	68	100.0	3541	4	US-10-296-734-1454	Sequence 1454, Ap
28	60	88.2	30	4	US-10-296-734-1436	Sequence 1436, Ap
29	60	88.2	135	4	US-10-295-027-388	Sequence 388, App
30	60	88.2	135	4	US-10-188-832-141	Sequence 141, App
31	60	88.2	180	4	US-10-146-473-69	Sequence 69, Appl
32	60	88.2	180	4	US-10-117-937-75	Sequence 75, Appl
33	60	88.2	180	4	US-10-296-734-834	Sequence 834, App
34	60	88.2	180	4	US-10-468-406-4	Sequence 4, Appli
35	60	88.2	180	4	US-10-657-022-75	Sequence 75, Appl
36	60	88.2	180	5	US-10-877-373-7	Sequence 7, Appli
37	60	88.2	180	6	US-11-067-064-75	Sequence 75, Appl
38	60	88.2	180	6	US-11-067-159-75	Sequence 75, Appl
39	60	88.2	210	4	US-10-157-031-88	Sequence 88, Appl
40	60	88.2	210	4	US-10-117-937-76	Sequence 76, Appl
41	60	88.2	210	4	US-10-657-022-76	Sequence 76, Appl
42	60	88.2	210	5	US-10-877-373-5	Sequence 5, Appli
43	60	88.2	210	6	US-11-067-064-76	Sequence 76, Appl
44	60	88.2	210	6	US-11-067-159-76	Sequence 76, Appl
45	56	82.4	20	4	US-10-313-986-496	Sequence 496, App

ALIGNMENTS

RESULT 1
US-10-296-734-1404
; Sequence 1404, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1404
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSO1a segment 4
US-10-296-734-1404

Query Match 100.0%; Score 68; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AARASGPGGGAPR 13
||||||||||||
Db 7 AARASGPGGGAPR 19

RESULT 2
US-10-482-029-202
; Sequence 202, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-202

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  Query Match             100.0%;  Score 68;  DB 5;  Length 179;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62


RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. US20020010321A1
;  GENERAL INFORMATION:
;    APPLICANT:  Stockert, Elisabeth; Jager, Elke;
;    APPLICANT:  Chen, Yao-tseng; Scanlan, Matthew;
;    APPLICANT:  Knuth, Alexander; Old, Lloyd J.
;    TITLE OF INVENTION:  Antibodies Which Bind to NY-ESO-1 Cancer
;    TITLE OF INVENTION:  Associated Proteins, Uses Thereof,
;    TITLE OF INVENTION:  Truncated Forms of NY-ESO-1, and HLA
;    TITLE OF INVENTION:  Binding Peptides Derived Therefrom
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/751,798
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/062,422
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. US20020010321A1man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3168
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-09-751-798-8

  Query Match             100.0%;  Score 68;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62


RESULT 4
US-09-849-602-30
; Sequence 30, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT:  Old, Lloyd J.
;  APPLICANT:  Stockert, Elisabeth
;  APPLICANT:  Chen, Yao-Tseng
;  TITLE OF INVENTION: Colon Cancer Antigen Panel
;  FILE REFERENCE: L0461/7105(JRV)
;  CURRENT APPLICATION NUMBER: US/09/849,602
;  CURRENT FILING DATE:  2001-05-04
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-849-602-30

  Query Match             100.0%;  Score 68;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62


RESULT 5
US-10-023-182-8
; Sequence 8, Application US/10023182
; Publication No. US20020164665A1
;   GENERAL INFORMATION:
;        APPLICANT: Stockert, Elisabeth; Jager, Elke;
;                   Chen, Yao-tseng; Scanlan, Matthew;
;                   Knuth, Alexander; Old, Lloyd J.
;        TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
;                            Associated Proteins, Uses Thereof,
;                            Truncated Forms of NY-ESO-1, and HLA
;                            Binding Peptides Derived Therefrom
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fulbright & Jaworski, L.L.P.
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10103
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: WordPerfect
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/023,182
;             FILING DATE: 17-Dec-2001
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/751,798
;             FILING DATE: December 29, 2000
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/725,182
;             FILING DATE: October 3, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, No. US20020164665A1man D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 5466.3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3168
;             TELEFAX: (212) 752-5958
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 180
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-023-182-8
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  Query Match           100.0%;  Score 68;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.37;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62


RESULT 6
US-10-207-655-71
; Sequence 71, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-207-655-71

  Query Match           100.0%;  Score 68;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.37;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
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Db         50 AARASGPGGGAPR 62


RESULT 7
US-10-364-614-14
; Sequence 14, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
;  APPLICANT: JAGER, Elke
;  APPLICANT:  KNUTH, Alexander
;  APPLICANT:  OLD, Lloyd
;  APPLICANT:  Gnjatic, Sacha
;  TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
;  FILE REFERENCE: LUD 5726.1 CIP
;  CURRENT APPLICATION NUMBER: US/10/364,614
;  CURRENT FILING DATE:  2003-02-24
;  PRIOR APPLICATION NUMBER: US 60/355,828
;  PRIOR FILING DATE: 2002-02-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-364-614-14

  Query Match           100.0%;  Score 68;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.37;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
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Db         50 AARASGPGGGAPR 62


RESULT 8
US-10-026-066-3
; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
; GENERAL INFORMATION:
;  APPLICANT: Simard, John J. L.
;  APPLICANT:  Diamond, David C.
;  TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
;  TITLE OF INVENTION:  PRESENTING CELLS
;  FILE REFERENCE: CTLIMM.21CP1C
;  CURRENT APPLICATION NUMBER: US/10/026,066
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: 09/561,074
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 09/560,465
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 09/561,572
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 09/561,571
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: PCT/US01/13806
;  PRIOR FILING DATE: 2001-04-27
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-026-066-3

  Query Match           100.0%;  Score 68;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.37;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
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Db         50 AARASGPGGGAPR 62


RESULT 9
US-10-117-937-74
; Sequence 74, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
;  APPLICANT: CTL IMMUNO THERAPIES CORP.
;  APPLICANT:  SIMARD, John, J.L.
;  APPLICANT:  DIAMOND, David, C.
;  APPLICANT:  LIU, Liping
;  APPLICANT:  XIE, Zhidong
;  TITLE OF INVENTION: EPITOPE SEQUENCES
;  FILE REFERENCE: CTLIMM.027A
;  CURRENT APPLICATION NUMBER: US/10/117,937
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: US 60/282,211
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/337,017
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: US 60/363,210
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 602
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-117-937-74

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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
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Db         50 AARASGPGGGAPR 62


RESULT 10
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US-10-295-027-386
; Sequence 386, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Ginsberg, Wendy M.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Glynne, Richard
;  APPLICANT:  Hevezi, Peter A.
;  APPLICANT:  Mack, David H.
;  APPLICANT:  Murray, Richard
;  APPLICANT:  Watson, Susan R.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;  TITLE OF INVENTION:  Methods of Screening for Modulators of Cancer
;  FILE REFERENCE: 018501-012500US
;  CURRENT APPLICATION NUMBER: US/10/295,027
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: US 09/663,733
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/335,394
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/332,464
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: US 60/334,393
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: US 60/340,376
;  PRIOR FILING DATE: 2001-12-14
;  PRIOR APPLICATION NUMBER: US 60/347,211
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: US 60/347,349
;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: US 60/355,250
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/356,714
;  PRIOR FILING DATE: 2002-02-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1386
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 386
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-295-027-386

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  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
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Db         50 AARASGPGGGAPR 62


RESULT 11
US-10-296-734-832
; Sequence 832, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
;  APPLICANT: Thompson, Scott A
;  APPLICANT:  Ramshaw, Ian A
;  TITLE OF INVENTION: Synthetic molecules and uses therefor
;  FILE REFERENCE: Savine
;  CURRENT APPLICATION NUMBER: US/10/296,734
;  CURRENT FILING DATE:  2003-08-04
;  PRIOR APPLICATION NUMBER: AU PQ7761/00
;  PRIOR FILING DATE: 2000-05-26
;  NUMBER OF SEQ ID NOS: 1507
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 832
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: NYNSO1a consensus polypeptide
US-10-296-734-832

  Query Match             100.0%;  Score 68;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
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Db         50 AARASGPGGGAPR 62


RESULT 12
US-10-188-832-139
; Sequence 139, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
;  APPLICANT: Mack, David H.
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
;  TITLE OF INVENTION:  and Methods of Screening for Modulators of Bladder
;  TITLE OF INVENTION:  Cancer
;  FILE REFERENCE: 018501-002330US
;  CURRENT APPLICATION NUMBER: US/10/188,832
;  CURRENT FILING DATE:  2002-11-22
;  PRIOR APPLICATION NUMBER: US 60/302,814
;  PRIOR FILING DATE: 2001-07-03
;  PRIOR APPLICATION NUMBER: US 60/310,099
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: US 60/343,705
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/372,246
;  PRIOR FILING DATE: 2002-04-12
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-188-832-139

  Query Match             100.0%;  Score 68;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62


RESULT 13
US-10-777-053-11
; Sequence 11, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
;  APPLICANT: Simard, John J. L.
;  APPLICANT:  Diamond, David C.
;  APPLICANT:  Qiu, Zhiyong
;  APPLICANT:  Lei, Xiang-Dong
;  TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
;  TITLE OF INVENTION:  TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
;  FILE REFERENCE: MANNK.022C1
;  CURRENT APPLICATION NUMBER: US/10/777,053
;  CURRENT FILING DATE:  2004-02-10
;  PRIOR APPLICATION NUMBER: 10/292,413
;  PRIOR FILING DATE: 2002-11-07
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;  PRIOR APPLICATION NUMBER: 60/336,968
;  PRIOR FILING DATE: 2001-11-07
;  NUMBER OF SEQ ID NOS: 979
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-777-053-11

  Query Match             100.0%;  Score 68;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62


RESULT 14
US-10-751-088-15
; Sequence 15, Application US/10751088
; Publication No. US20040158044A1
;   GENERAL INFORMATION:
;        APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
;                   Gure, Ali, Old, Lloyd, Ritter, Gerd
;        TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                            SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
;                            USES THEREOF
;        NUMBER OF SEQUENCES: 15
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FULBRIGHT & JAWORSKI LLP
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10158
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/751,088
;             FILING DATE: 02-Jan-2004
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/165,546D
;             FILING DATE: 02-Oct-1998
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: April 17, 1998
;             APPLICATION NUMBER: 08/937,263
;             FILING DATE: September 15, 1997
;             APPLICATION NUMBER: US 08/725,182
;             FILING DATE: October 3, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, Norman D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3000
;             TELEFAX: (212) 318-3400
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 180 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-10-751-088-15

  Query Match             100.0%;  Score 68;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62


RESULT 15
US-10-657-022-74
; Sequence 74, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
;  APPLICANT: Simard, John J. L.
;  APPLICANT:  Diamond, David C.
;  APPLICANT:  Liu, Liping
;  APPLICANT:  Liu, Zheng
;  TITLE OF INVENTION: EPITOPE SEQUENCES
;  FILE REFERENCE: MANNK.032A
;  CURRENT APPLICATION NUMBER: US/10/657,022
;  CURRENT FILING DATE:  2003-09-04
;  PRIOR APPLICATION NUMBER: 60/409123
;  PRIOR FILING DATE: 2002-09-06
;  NUMBER OF SEQ ID NOS: 610
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-657-022-74

  Query Match             100.0%;  Score 68;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||||||||||||
Db         50 AARASGPGGGAPR 62


Search completed: March 13, 2006, 20:02:27
Job time : 78.6118 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:54:06 ; Search time 8.87059 Seconds
(without alignments)
40.793 Million cell updates/sec

Title: US-09-529-206E-28
Perfect score: 68
Sequence: 1 AARASGPGGGAPR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	68	100.0	180	7	US-11-155-288-7	Sequence 7, Appli
2	68	100.0	240	7	US-11-021-441-28	Sequence 28, Appl
3	56	82.4	20	6	US-10-623-155-496	Sequence 496, App
4	47	69.1	306	7	US-11-096-568A-20556	Sequence 20556, A
5	47	69.1	353	7	US-11-096-568A-22334	Sequence 22334, A
6	47	69.1	358	7	US-11-096-568A-22333	Sequence 22333, A
7	47	69.1	420	7	US-11-096-568A-22332	Sequence 22332, A
8	46	67.6	134	7	US-11-096-568A-23806	Sequence 23806, A
9	45	66.2	678	7	US-11-072-512-3295	Sequence 3295, Ap
10	44	64.7	379	7	US-11-109-156-16	Sequence 16, Appl
11	44	64.7	558	7	US-11-096-568A-26217	Sequence 26217, A
12	44	64.7	974	6	US-10-531-036-35	Sequence 35, Appl
13	43	63.2	413	7	US-11-096-568A-27265	Sequence 27265, A
14	42	61.8	162	7	US-11-096-568A-641	Sequence 641, App
15	42	61.8	249	7	US-11-096-568A-23045	Sequence 23045, A
16	41.5	61.0	167	7	US-11-096-568A-10542	Sequence 10542, A
17	41	60.3	119	7	US-11-110-424-4	Sequence 4, Appli
18	41	60.3	268	7	US-11-087-099-6009	Sequence 6009, Ap
19	41	60.3	306	7	US-11-100-640-26	Sequence 26, Appl
20	41	60.3	365	7	US-11-108-528-58	Sequence 58, Appl
21	41	60.3	537	7	US-11-179-958A-2	Sequence 2, Appli
22	41	60.3	555	7	US-11-072-512-3369	Sequence 3369, Ap
23	41	60.3	953	7	US-11-037-243-66	Sequence 66, Appl
24	40.5	59.6	280	7	US-11-143-980-34	Sequence 34, Appl
25	40	58.8	291	7	US-11-087-099-3763	Sequence 3763, Ap
26	40	58.8	1832	7	US-11-087-099-7762	Sequence 7762, Ap
27	39	57.4	178	7	US-11-096-568A-20715	Sequence 20715, A
28	39	57.4	213	7	US-11-072-512-2722	Sequence 2722, Ap
29	39	57.4	228	7	US-11-096-568A-22508	Sequence 22508, A
30	39	57.4	233	7	US-11-240-769-58	Sequence 58, Appl
31	39	57.4	284	7	US-11-096-568A-11286	Sequence 11286, A
32	39	57.4	298	6	US-10-821-234-1240	Sequence 1240, Ap
33	39	57.4	430	6	US-10-992-577-8	Sequence 8, Appli
34	39	57.4	430	6	US-10-508-892-2	Sequence 2, Appli
35	39	57.4	430	7	US-11-223-294-54	Sequence 54, Appl
36	39	57.4	461	7	US-11-096-568A-18223	Sequence 18223, A
37	39	57.4	493	7	US-11-096-568A-18222	Sequence 18222, A
38	39	57.4	496	7	US-11-096-568A-18221	Sequence 18221, A
39	39	57.4	618	7	US-11-078-735-18	Sequence 18, Appl
40	39	57.4	618	7	US-11-050-346-63	Sequence 63, Appl
41	39	57.4	618	7	US-11-103-077-18	Sequence 18, Appl
42	39	57.4	662	7	US-11-072-175-184	Sequence 184, App
43	39	57.4	736	7	US-11-078-189-11	Sequence 11, Appl
44	39	57.4	830	6	US-10-921-793-38	Sequence 38, Appl
45	39	57.4	830	6	US-10-931-198-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-11-155-288-7
; Sequence 7, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-7

Query Match 100.0%; Score 68; DB 7; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AARASGPGGGAPR 13
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Db 50 AARASGPGGGAPR 62

RESULT 2
US-11-021-441-28
; Sequence 28, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616;750
; PRIOR FILING DATE: 2004-10-06

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;  PRIOR APPLICATION NUMBER: US 60/615,287
;  PRIOR FILING DATE: 2004-10-01
;  PRIOR APPLICATION NUMBER: US 60/599,377
;  PRIOR FILING DATE: 2004-08-05
;  PRIOR APPLICATION NUMBER: PCT/US2004/23881
;  PRIOR FILING DATE: 2004-07-23
;  PRIOR APPLICATION NUMBER: US 10/883,599
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: US 60/556,744
;  PRIOR FILING DATE: 2004-03-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion protein
US-11-021-441-28

  Query Match             100.0%;  Score 68;  DB 7;  Length 240;
  Best Local Similarity   100.0%;  Pred. No. 0.014;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
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Db        110 AARASGPGGGAPR 122


RESULT 3
US-10-623-155-496
; Sequence 496, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Peckham, David W.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C20
;  CURRENT APPLICATION NUMBER: US/10/623,155
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 496
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-623-155-496

  Query Match             82.4%;  Score 56;  DB 6;  Length 20;
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  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGA 11
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Db         10 AARASGPGGGA 20


RESULT 4
US-11-096-568A-20556
; Sequence 20556, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20556
;   LENGTH: 306
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(306)
;   OTHER INFORMATION: Ceres Seq. ID no. 12383286
US-11-096-568A-20556

  Query Match             69.1%;  Score 47;  DB 7;  Length 306;
  Best Local Similarity   81.8%;  Pred. No. 11;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 ARASGPGGGAP 12
              ||| ||| |||
Db         91 ARADGPGTGAP 101


RESULT 5
US-11-096-568A-22334
; Sequence 22334, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22334
;   LENGTH: 353
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(353)
;   OTHER INFORMATION: Ceres Seq. ID no. 12408544
US-11-096-568A-22334

  Query Match             69.1%;  Score 47;  DB 7;  Length 353;
  Best Local Similarity   69.2%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||  ||||  ||
Db        108 AARGQGPGGEQPR 120


RESULT 6
US-11-096-568A-22333
; Sequence 22333, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22333
;   LENGTH: 358
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(358)
;   OTHER INFORMATION: Ceres Seq. ID no. 12408543
US-11-096-568A-22333

  Query Match             69.1%;  Score 47;  DB 7;  Length 358;
  Best Local Similarity   69.2%;  Pred. No. 13;
```

```
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||  ||||  ||
Db        113 AARGQGPGGEQPR 125


RESULT 7
US-11-096-568A-22332
; Sequence 22332, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22332
;   LENGTH: 420
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(420)
;   OTHER INFORMATION: Ceres Seq. ID no. 12408542
US-11-096-568A-22332

  Query Match             69.1%;  Score 47;  DB 7;  Length 420;
  Best Local Similarity   69.2%;  Pred. No. 15;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||  ||||  ||
Db        175 AARGQGPGGEQPR 187


RESULT 8
US-11-096-568A-23806
; Sequence 23806, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23806
;   LENGTH: 134
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(134)
;   OTHER INFORMATION: Ceres Seq. ID no. 12415289
US-11-096-568A-23806

  Query Match             67.6%;  Score 46;  DB 7;  Length 134;
  Best Local Similarity   72.7%;  Pred. No. 7.3;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 ARASGPGGGAP 12
              || :||| |||
Db         69 ARGAGPGAGAP 79


RESULT 9
US-11-072-512-3295
; Sequence 3295, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
;  APPLICANT: ISOGAI, TAKAO
;  APPLICANT:  SUGIYAMA, TOMOYASU
;  APPLICANT:  OTSUKI, TETSUJI
;  APPLICANT:  WAKAMATSU, AI
;  APPLICANT:  SATO, HIROYUKI
;  APPLICANT:  ISHII, SHIZUKO
;  APPLICANT:  YAMAMOTO, JUN-ICHI
;  APPLICANT:  ISONO, YUUKO
;  APPLICANT:  HIO, YURI
;  APPLICANT:  OTSUKA, KAORU
;  APPLICANT:  NAGAI, KEIICHI
;  APPLICANT:  IRIE, RYOTARO
;  APPLICANT:  TAMECHIKA, ICHIRO
;  APPLICANT:  SEKI, NAOHIKO
;  APPLICANT:  YOSHIKAWA, TSUTOMU
;  APPLICANT:  OTSUKA, MOTOYUKI
;  APPLICANT:  NAGAHARI, KENJI
;  APPLICANT:  MASUHO, YASUHIKO
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: 084335-0191
;  CURRENT APPLICATION NUMBER: US/11/072,512
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: US 60/350,978
;  PRIOR FILING DATE: 2002-01-25
;  PRIOR APPLICATION NUMBER: JP 2001-379298
;  PRIOR FILING DATE: 2001-11-05
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3295
;   LENGTH: 678
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-072-512-3295

  Query Match             66.2%;  Score 45;  DB 7;  Length 678;
  Best Local Similarity   80.0%;  Pred. No. 41;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 RASGPGGGAP 12
              ||:||||| |
Db        592 RAAGPGGGWP 601


RESULT 10
US-11-109-156-16
; Sequence 16, Application US/11109156
; Publication No. US20050250144A1
; GENERAL INFORMATION:
;  APPLICANT: Toshio Ota
;  APPLICANT:  Takao Isogai
;  APPLICANT:  Tetsuo Nishikawa
;  APPLICANT:  Koji Hayashi
;  APPLICANT:  Kaoru Otsuka
;  APPLICANT:  Jun-Ichi Yamamoto
;  APPLICANT:  Shizuko Ishii
;  APPLICANT:  Tomoyasu Sugiyama
;  APPLICANT:  Ai Wakamatsu
;  APPLICANT:  Keiichi Nagai
;  APPLICANT:  Tetsuji Otsuki
;  APPLICANT:  Shin-Ichi Funahashi
;  APPLICANT:  Chiaki Senoo
;  APPLICANT:  Jun-Ichi Nezu
;  TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
;  TITLE OF INVENTION:  PHOSPHATASE
;  FILE REFERENCE: 06501-099002
;  CURRENT APPLICATION NUMBER: US/11/109,156
;  CURRENT FILING DATE:  2005-04-19
;  PRIOR APPLICATION NUMBER: US/10/060,065
;  PRIOR FILING DATE: 2002-01-29
;  PRIOR APPLICATION NUMBER: PCT/JP00/05061
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: US 60/159,590
```

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;  PRIOR FILING DATE: 1999-10-18
;  PRIOR APPLICATION NUMBER: US 60/183,322
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: JP 11-248036
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: JP 2000-118776
;  PRIOR FILING DATE: 2000-01-11
;  PRIOR APPLICATION NUMBER: JP 2000-183767
;  PRIOR FILING DATE: 2000-05-02
;  PRIOR APPLICATION NUMBER: JP 2000-241899
;  PRIOR FILING DATE: 2000-06-09
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
;   LENGTH: 379
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-109-156-16

  Query Match             64.7%;  Score 44;  DB 7;  Length 379;
  Best Local Similarity   69.2%;  Pred. No. 33;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              || | | ||| ||
Db          3 AAAAQGGGGGEPR 15


RESULT 11
US-11-096-568A-26217
; Sequence 26217, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26217
;   LENGTH: 558
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(558)
;   OTHER INFORMATION: Ceres Seq. ID no. 13498878
US-11-096-568A-26217

  Query Match             64.7%;  Score 44;  DB 7;  Length 558;
  Best Local Similarity   66.7%;  Pred. No. 47;
  Matches    8;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ARASGPGGGAPR 13
              ||  || || ||
Db        389 ARQEGPAGGEPR 400


RESULT 12
US-10-531-036-35
; Sequence 35, Application US/10531036
; Publication No. US20060015951A1
; GENERAL INFORMATION:
;  APPLICANT: Eulenberg, Karsten
;  APPLICANT:  Meise, Martin
;  APPLICANT:  Molitor, Andreas
;  APPLICANT:  Steuernagel, Arnd
;  TITLE OF INVENTION: Proteins Involved in the Regulation of Energy Homeostasis
;  FILE REFERENCE: 2923-696
;  CURRENT APPLICATION NUMBER: US/10/531,036
;  CURRENT FILING DATE:  2005-04-12
;  PRIOR APPLICATION NUMBER: PCT/EP03/11352
;  PRIOR FILING DATE: 2003-10-14
;  PRIOR APPLICATION NUMBER: EP 02024747.4
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: EP 02023560.2
;  PRIOR FILING DATE: 2002-10-22
;  PRIOR APPLICATION NUMBER: EP 02022880.5
;  PRIOR FILING DATE: 2002-10-14
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
;   LENGTH: 974
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-531-036-35

  Query Match             64.7%;  Score 44;  DB 6;  Length 974;
  Best Local Similarity   71.4%;  Pred. No. 76;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    1;

Qy          1 AARASG--PGGGAP 12
              | || |  ||||||
Db          4 AGRAGGPPPGGGAP 17


RESULT 13
US-11-096-568A-27265
; Sequence 27265, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27265
;   LENGTH: 413
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(413)
;   OTHER INFORMATION: Ceres Seq. ID no. 15180691
US-11-096-568A-27265

  Query Match             63.2%;  Score 43;  DB 7;  Length 413;
  Best Local Similarity   72.7%;  Pred. No. 49;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ARASGPGGGAP 12
              ||  |||| ||
Db         95 ARRRGPGGAAP 105


RESULT 14
US-11-096-568A-641
; Sequence 641, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 641
;   LENGTH: 162
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
```

```
;   LOCATION: (1)..(162)
;   OTHER INFORMATION: Ceres Seq. ID no. 12635935
US-11-096-568A-641

  Query Match             61.8%;  Score 42;  DB 7;  Length 162;
  Best Local Similarity   66.7%;  Pred. No. 30;
  Matches    8;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAP 12
              |||: | ||| |
Db         41 AARSGGGGGGRP 52


RESULT 15
US-11-096-568A-23045
; Sequence 23045, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23045
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(249)
;   OTHER INFORMATION: Ceres Seq. ID no. 12411110
US-11-096-568A-23045

  Query Match             61.8%;  Score 42;  DB 7;  Length 249;
  Best Local Similarity   69.2%;  Pred. No. 43;
  Matches    9;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AARASGPGGGAPR 13
              |||  | |||| |
Db         18 AARGKGGGGGANR 30


Search completed: March 13, 2006, 20:03:31
Job time : 9.87059 secs
```

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 18:52:59 ; Search time 90.3529 Seconds
(without alignments)
58.355 Million cell updates/sec

Title: US-09-529-206E-29
Perfect score: 64
Sequence: 1 ARASGPGGGAPR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	64	100.0	12	2	AAY06065	Aay06065 Human can
2	64	100.0	13	2	AAY06064	Aay06064 Human can
3	64	100.0	14	2	AAY05986	Aay05986 Human can
4	64	100.0	15	2	AAY05978	Aay05978 Human can
5	64	100.0	20	2	AAY05979	Aay05979 Human can
6	64	100.0	30	5	AAU85105	Aau85105 Human NYN
7	64	100.0	179	8	ADK68648	Adk68648 Epitope l
8	64	100.0	180	2	AAW62584	Aaw62584 Cancer as
9	64	100.0	180	2	AAW69665	Aaw69665 Human NY-
10	64	100.0	180	2	AAY05965	Aay05965 Human can
11	64	100.0	180	3	AAY52430	Aay52430 Human tum
12	64	100.0	180	3	AAY70862	Aay70862 Human tum
13	64	100.0	180	3	AAB03154	Aab03154 Human oes
14	64	100.0	180	4	AAB69946	Aab69946 Human NY-
15	64	100.0	180	4	AAG67164	Aag67164 Amino aci
16	64	100.0	180	4	AAU01535	Aau01535 Human NY-
17	64	100.0	180	4	AAE07714	Aae07714 Human NY
18	64	100.0	180	5	AAU84818	Aau84818 Human NYN
19	64	100.0	180	5	AAU11543	Aau11543 Human tum
20	64	100.0	180	6	ABR58672	Abr58672 Human can
21	64	100.0	180	6	ABR48210	Abr48210 Human bla
22	64	100.0	180	6	ABU56508	Abu56508 Lung canc
23	64	100.0	180	6	ABU56694	Abu56694 Lung canc
24	64	100.0	180	6	ABP74198	Abp74198 Human NY-
25	64	100.0	180	6	ABU64816	Abu64816 Human NY-
26	64	100.0	180	6	ABR83438	Abr83438 Human NY-
27	64	100.0	180	7	ADC09576	Adc09576 NY-ESO-1
28	64	100.0	180	7	ADD35564	Add35564 Human NY-
29	64	100.0	180	7	ADD35568	Add35568 Human NY-
30	64	100.0	180	7	ADD25510	Add25510 Binding d
31	64	100.0	180	7	ADN39068	Adn39068 Cancer/an
32	64	100.0	180	8	ADJ54139	Adj54139 Human NY-
33	64	100.0	180	8	ADM72815	Adm72815 Human NY-
34	64	100.0	180	8	ADM73418	Adm73418 CAG-3 pro
35	64	100.0	180	8	ADM73417	Adm73417 Human NY-
36	64	100.0	180	8	ADQ18451	Adq18451 Human sof
37	64	100.0	180	8	ADQ10446	Adq10446 Autoimmun
38	64	100.0	180	8	ADS80926	Ads80926 Tumour as
39	64	100.0	180	9	ADW44353	Adw44353 Human aut
40	64	100.0	180	9	ADY85096	Ady85096 Tumor ant
41	64	100.0	180	9	ADZ28913	Adz28913 NY-ESO-1
42	64	100.0	180	9	ADZ42374	Adz42374 Immunogen
43	64	100.0	180	9	AEA35651	Aea35651 Human NY-
44	64	100.0	240	9	ADW99402	Adw99402 NY-ESO-1/
45	64	100.0	240	9	AEB80047	Aeb80047 Human NY-

ALIGNMENTS

RESULT 1
AAY06065
ID AAY06065 standard; peptide; 12 AA.
XX
AC AAY06065;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 peptide.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Example 11; Page 50; 88pp; English.
XX
CC This peptide corresponds to amino acid residues 51-62 of human NY ESO-
CC 1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is
CC capable of eliciting an antigen specific immune response by T cells.
CC Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3
CC and their variants, are useful as cancer vaccines. A claimed method of
CC preventing or inhibiting cancer involves administering a cancer peptide,
CC with or without an HLA molecule. The cancer peptides form part of, or are
CC derived from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,

```
CC   cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC   as breast, prostate, ovarian, pancreatic and thyroid cancers
XX
SQ   Sequence 12 AA;

  Query Match             100.0%;  Score 64;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0.049;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db          1 ARASGPGGGAPR 12


RESULT 2
AAY06064
ID   AAY06064 standard; peptide; 13 AA.
XX
AC   AAY06064;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 peptide.
XX
KW   NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW   leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW   metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW   uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW   cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW   liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW   vaccine; cytotoxic T lymphocyte; CTL.
XX
OS   Homo sapiens.
XX
PN   WO9918206-A2.
XX
PD   15-APR-1999.
XX
PF   21-SEP-1998;   98WO-US019609.
XX
PR   08-OCT-1997;   97US-0061428P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang RF,  Rosenberg SA;
XX
DR   WPI; 1999-277270/23.
XX
PT   Cancer antigen NY ESO1/CAG-3.
XX
PS   Example 11; Page 50; 88pp; English.
XX
CC   This peptide corresponds to amino acid residues 50-62 of human NY ESO-
CC   1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is
CC   capable of eliciting an antigen specific immune response by T cells.
CC   Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3
CC   and their variants, are useful as cancer vaccines. A claimed method of
CC   preventing or inhibiting cancer involves administering a cancer peptide,
CC   with or without an HLA molecule. The cancer peptides form part of, or are
CC   derived from, cancers such as primary or metastatic melanoma, thymoma,
CC   lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC   cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC   as breast, prostate, ovarian, pancreatic and thyroid cancers
XX
SQ   Sequence 13 AA;

  Query Match             100.0%;  Score 64;  DB 2;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0.052;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db          2 ARASGPGGGAPR 13


RESULT 3
AAY05986
ID   AAY05986 standard; peptide; 14 AA.
XX
AC   AAY05986;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
KW   NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW   leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW   metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW   uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW   cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW   liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW   vaccine.
XX
OS   Homo sapiens.
XX
PN   WO9918206-A2.
XX
PD   15-APR-1999.
XX
PF   21-SEP-1998;   98WO-US019609.
XX
PR   08-OCT-1997;   97US-0061428P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang RF,  Rosenberg SA;
XX
DR   WPI; 1999-277270/23.
XX
PT   Cancer antigen NY ESO1/CAG-3.
XX
PS   Claim 25; Page 50; 88pp; English.
XX
CC   The present sequence represents a cancer peptide that corresponds to
CC   amino acid residues 49-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
CC   AAY05965), a new and potent tumour antigen capable of eliciting an
CC   antigen specific immune response by T cells. Cancer peptides derived from
CC   CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
CC   variants (see AAY05967-87), are useful as cancer vaccines that protect
CC   against cancer. The invention provides: vectors and host cells (also
CC   useful as vaccines); a method of diagnosis of cancer or precancer; a
CC   transgenic animal; antisense oligonucleotides that inhibit expression of
CC   the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
CC   cancer peptide, useful in diagnostic and detection assays; and methods
CC   for preventing or inhibiting cancer by administering a cancer peptide,
CC   with or without an HLA molecule. The cancer peptides form part of, or are
CC   derived from, cancers such as primary or metastatic melanoma, thymoma,
CC   lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC   cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC   as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
CC   treated by inducing cancer-specific T cells in vitro for subsequent
CC   return to a patient
XX
SQ   Sequence 14 AA;

  Query Match             100.0%;  Score 64;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0.056;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db          3 ARASGPGGGAPR 14


RESULT 4
AAY05978
```

```
ID   AAY05978 standard; peptide; 15 AA.
XX
AC   AAY05978;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
KW   NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW   leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW   metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW   uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW   cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW   liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW   vaccine.
XX
OS   Homo sapiens.
XX
PN   WO9918206-A2.
XX
PD   15-APR-1999.
XX
PF   21-SEP-1998;   98WO-US019609.
XX
PR   08-OCT-1997;   97US-0061428P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang RF,  Rosenberg SA;
XX
DR   WPI; 1999-277270/23.
XX
PT   Cancer antigen NY ESO1/CAG-3.
XX
PS   Claim 15; Page 64; 88pp; English.
XX
CC   The present sequence represents a cancer peptide that corresponds to
CC   amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
CC   AAY05965), a new and potent tumour antigen capable of eliciting an
CC   antigen specific immune response by T cells. Cancer peptides derived from
CC   CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
CC   variants (see AAY05967-87), are useful as cancer vaccines that protect
CC   against cancer. The invention provides: vectors and host cells (also
CC   useful as vaccines); a method of diagnosis of cancer or precancer; a
CC   transgenic animal; antisense oligonucleotides that inhibit expression of
CC   the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
CC   cancer peptide, useful in diagnostic and detection assays; and methods
CC   for preventing or inhibiting cancer by administering a cancer peptide,
CC   with or without an HLA molecule. The cancer peptides form part of, or are
CC   derived from, cancers such as primary or metastatic melanoma, thymoma,
CC   lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC   cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC   as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
CC   treated by inducing cancer-specific T cells in vitro for subsequent
CC   return to a patient
XX
SQ   Sequence 15 AA;

  Query Match             100.0%;  Score 64;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.059;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db          4 ARASGPGGGAPR 15


RESULT 5
AAY05979
ID   AAY05979 standard; peptide; 20 AA.
XX
AC   AAY05979;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
KW   NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW   leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW   metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW   uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW   cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW   liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW   vaccine.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9918206-A2.
XX
PD   15-APR-1999.
XX
PF   21-SEP-1998;   98WO-US019609.
XX
PR   08-OCT-1997;   97US-0061428P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang RF,  Rosenberg SA;
XX
DR   WPI; 1999-277270/23.
XX
PT   Cancer antigen NY ESO1/CAG-3.
XX
PS   Claim 16; Page 64; 88pp; English.
XX
CC   The present sequence represents a cancer peptide that is based on amino
CC   acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965),
CC   a new and potent tumour antigen capable of eliciting an antigen specific
CC   immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-
CC   3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-
CC   87), are useful as cancer vaccines that protect against cancer. The
CC   invention provides: vectors and host cells (also useful as vaccines); a
CC   method of diagnosis of cancer or precancer; a transgenic animal;
CC   antisense oligonucleotides that inhibit expression of the cancer peptide
CC   or tumour antigen; antibodies reacting with a CAG-3 cancer peptide,
CC   useful in diagnostic and detection assays; and methods for preventing or
CC   inhibiting cancer by administering a cancer peptide, with or without an
CC   HLA molecule. The cancer peptides form part of, or are derived from,
CC   cancers such as primary or metastatic melanoma, thymoma, lymphoma,
CC   sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
CC   cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
CC   prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by
CC   inducing cancer-specific T cells in vitro for subsequent return to a
CC   patient
XX
SQ   Sequence 20 AA;

  Query Match             100.0%;  Score 64;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.076;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db          9 ARASGPGGGAPR 20


RESULT 6
AAU85105
ID   AAU85105 standard; peptide; 30 AA.
XX
AC   AAU85105;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Human NYNSO1a segment 4.
```

XX
KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW viral infection; human immunodeficieny virus; melanoma;
KW bacterial infection; Salmonella; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
XX
OS Homo sapiens.
XX
PN WO200190197-A1.
XX
PD 29-NOV-2001.
XX
PF 25-MAY-2001; 2001WO-AU000622.
XX
PR 26-MAY-2000; 2000AU-00007761.
XX
PA (AUSU) UNIV AUSTRALIAN NAT.
XX
PI Thomson SA, Ramshaw IA;
XX
DR WPI; 2002-147575/19.
DR N-PSDB; ABK36925.
XX
PT New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
PS Example 3; Fig 27; 364pp; English.
XX
CC The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention
XX
SQ Sequence 30 AA;

Query Match 100.0%; Score 64; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARASGPGGGAPR 12
||||||||||||
Db 8 ARASGPGGGAPR 19

RESULT 7
ADK68648
ID ADK68648 standard; protein; 179 AA.
XX
AC ADK68648;
XX
DT 06-MAY-2004 (first entry)
XX
DE Epitope liberation-related NY-ESO-1 protein SeqID11.
XX
KW epitope liberation; substrate; proteasome; cytostatic; antibacterial;
KW protozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope;
KW cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;
KW virus; bacterium; protozoan; fungus; housekeeping proteasome system;
KW human.
XX
OS Homo sapiens.
XX
PN US2003228634-A1.
XX
PD 11-DEC-2003.
XX
PF 07-NOV-2002; 2002US-00292413.
XX
PR 07-NOV-2001; 2001US-0336968P.
XX
PA (SIMA/) SIMARD J J L.
PA (DIAM/) DIAMOND D C.
PA (QIUZ/) QIU Z.
PA (LEIX/) LEI X.
XX
PI Simard JJL, Diamond DC, Qiu Z, Lei X;
XX
DR WPI; 2004-167209/16.
DR N-PSDB; ADK68674.
XX
PT Identifying polypeptide suitable for epitope e.g., housekeeping epitope,
PT liberation by contacting substrate polypeptide comprising epitope of
PT interest, with proteasome, and assaying for liberation of epitope.
XX
PS Example 2; SEQ ID NO 11; 67pp; English.
XX
CC This invention relates to a novel method of identifying a polypeptide
CC suitable for epitope liberation, including the steps of identifying an
CC epitope of interest; providing substrate polypeptide sequence including
CC the epitope, wherein the substrate permits processing by a proteasome;
CC contacting the substrate with a composition including the proteasome,
CC under conditions that support processing of the substrate by proteasome;
CC and assaying for liberation of epitope. The invention may be useful for
CC the development of compounds with a cytostatic, antibacterial,
CC protozoacide or fungicide activity acting as T-cell activators. In
CC addition, the invention may allow development of a vaccine. The invention
CC is useful for identifying a polypeptide suitable for epitope liberation,
CC where the epitope is a housekeeping epitope. The compositions comprising
CC the identified housekeeping epitopes are useful in vitro in vaccine
CC development or in the generation or expansion of cytotoxic T lymphocyte
CC (CTL) to be used in adoptive immunotherapy. The invention is also useful
CC for activating T-cells against neoplastic cells, and cells infected with
CC virus, bacterium, protozoan or fungus. CTL epitopes are identified based
CC on the knowledge that such epitopes are, in fact, produced by the
CC housekeeping proteasome system. Once identified, these epitopes, embodied
CC as peptides, can be used to successfully immunise or induce therapeutic
CC CTL responses against housekeeping proteasome expressing target cells in
CC the host. The present sequence is that of a protein which is related to
CC the method of the invention.
XX
SQ Sequence 179 AA;

Query Match 100.0%; Score 64; DB 8; Length 179;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARASGPGGGAPR 12
||||||||||||
Db 50 ARASGPGGGAPR 61

RESULT 8
AAW62584
ID AAW62584 standard; protein; 180 AA.
XX

```
AC   AAW62584;
XX
DT   17-SEP-1998  (first entry)
XX
DE   Cancer associated antigen NY-ESO-1.
XX
KW   Cancer associated antigen; NY-ESO-1; regression; progression; onset;
KW   cancer; treatment; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 7
FT                   /note= "potential myristorylation site"
FT   Misc-difference 9
FT                   /note= "potential myristorylation site"
FT   Misc-difference 11
FT                   /note= "potential phosphorylation site"
FT   Misc-difference 98
FT                   /note= "potential phosphorylation site"
FT   Misc-difference 134
FT                   /note= "potential phosphorylation site"
FT   Misc-difference 138
FT                   /note= "potential phosphorylation site"
XX
PN   WO9814464-A1.
XX
PD   09-APR-1998.
XX
PF   15-SEP-1997;   97WO-US016335.
XX
PR   03-OCT-1996;   96US-00725182.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Chen Y,  Scanlan M,  Gure A,  Old LJ,  Jager E,  Knuth A;
PI   Drijfhout JW;
XX
DR   WPI; 1998-286417/25.
DR   N-PSDB; AAV38566.
XX
PT   New isolated cancer associated antigen - is used to develop products for
PT   the diagnosis and treatment of cancers and for monitoring cancer therapy.
XX
PS   Claim 8; Fig 3; 49pp; English.
XX
CC   The present sequence represents a cancer associated antigen. The clone
CC   from which the DNA sequence is obtained is designated NY-ESO-1. The
CC   specification described a method for determining regression, progression
CC   of onset of a cancerous condition, comprising monitoring a sample from a
CC   patient with the cancerous condition for a parameter selected from NY-ESO
CC   -1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells
CC   specific for the peptide and an MHC molecule with which it non-covalently
CC   complexes. Methods for the treatment of a cancerous condition are also
CC   described. The NY-ESO-1 protein and peptides derived from it can be used
CC   for diagnosis and treatment of cancers and to monitor the efficacy of a
CC   therapeutic regime
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 64;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.51;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 9
AAW69665
ID   AAW69665 standard; protein; 180 AA.
XX
AC   AAW69665;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
XX
KW   Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
XX
OS   Homo sapiens.
XX
PN   WO9832855-A1.
XX
PD   30-JUL-1998.
XX
PF   27-JAN-1998;   98WO-US001445.
XX
PR   27-JAN-1997;   97US-00791495.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Lethe B,  Lucas S,  De Smet C,  Godelaine D,  Boon-Falleur T;
XX
DR   WPI; 1998-427951/36.
DR   N-PSDB; AAV50348.
XX
PT   New isolated LAGE-1 tumour associated nucleic acids - used to develop
PT   products for the diagnosis and treatment of LAGE-1 associated disorders,
PT   particularly tumours.
XX
PS   Example 2; Page 57-58; 73pp; English.
XX
CC   The present sequence represents human NY-ESO-1, formerly known as LL-1.2
CC   clone, which is used in an example from the present invention which
CC   describes LAGE-1 tumour associated protein (TAP). The present invention
CC   also describes: (1) a method for treating a subject with a disorder
CC   characterised by expression of a LAGE-1 nucleic acid molecule or an
CC   expression product, comprising administering to the subject autologous
CC   cytolytic T cells to ameliorate the disorder, where the cytolytic T cells
CC   are specific for complexes of an HLA molecule and a LAGE-1 TAP or an
CC   immunogenic fragment; (2) a method for treating a subject with a disorder
CC   characterised by expression of a LAGE-1 nucleic acid molecule or an
CC   expression product, comprising administering a LAGE-1 TAP or an
CC   immunogenic fragment to ameliorate the disorder; and (3) a method for
CC   selectively enriching a population of T cells with cytolytic T cells
CC   specific for a LAGE-1 TAP comprising contacting an isolated population of
CC   T cells with an agent presenting a complex of a LAGE TAP or an
CC   immunogenic fragment and a HLA presenting molecule to selectively enrich
CC   the isolated population of T cells with the cytolytic T cells. The
CC   methods and products from the present invention can be used for the
CC   diagnosis and treatment of LAGE-1 associated disorders, particularly
CC   tumours
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 64;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.51;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 10
AAY05965
ID   AAY05965 standard; protein; 180 AA.
XX
AC   AAY05965;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.
XX
```

KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia;
KW non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis;
KW melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer;
KW breast cancer; prostate cancer; ovarian cancer; cervical cancer;
KW bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma;
KW tumour; diagnosis; immunotherapy; therapy; vaccine; ORF1.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
DR N-PSDB; AAX58599.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Claim 4; Fig 3A; 88pp; English.
XX
CC The present sequence represents the ORF1 protein encoded by open reading
CC frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and
CC potent tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides comprising ORF1, ORF2 (see
CC AAY05966), portions of these peptides and their variants (see AAY05965-
CC 87), are useful as cancer vaccines that protect the recipient from
CC development of cancer. The invention provides: vectors and host cells
CC (also useful as vaccines); a method of diagnosis of cancer or precancer;
CC a transgenic animal; antisense oligonucleotides that inhibit expression
CC of the cancer peptide or tumour antigen; antibodies reacting with the CAG
CC -3 cancer peptide, useful in diagnostic and detection assays; and methods
CC for preventing or inhibiting cancer by administering a cancer peptide,
CC with or without an HLA molecule. The cancer peptides form part of, or are
CC derived from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
CC treated by inducing cancer-specific T cells in vitro for subsequent
CC return to a patient
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 64; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARASGPGGGAPR 12
||||||||||||
Db 51 ARASGPGGGAPR 62

RESULT 11
AAY52430
ID AAY52430 standard; protein; 180 AA.
XX
AC AAY52430;
XX
DT 21-OCT-2004 (revised)
DT 15-FEB-2000 (first entry)
XX
DE Human tumour antigen NY-ESO-1.
XX
KW Cancer; tumour; antigen; MHC; major histocompatility complex; T-cell;
KW cytotoxic; helper; stimulation; proliferation; treatment; diagnosis;
KW prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;
KW hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
XX
OS Homo sapiens.
OS Unidentified.
XX

FH	Key	Location/Qualifiers
FT	Peptide	44. .53
FT		/note= "Peptide presented by MHC Class I HLA-B7"
FT	Peptide	60. .69
FT		/note= "Peptide presented by MHC Class I HLA-B7"
FT	Peptide	60. .68
FT		/note= "Peptide presented by MHC Class I HLA-B7"
FT	Peptide	63. .72
FT		/note= "Peptide presented by MHC Class I HLA-B7"
FT	Peptide	79. .88
FT		/note= "Peptide presented by MHC Class I HLA-B7"
FT	Peptide	79. .87
FT		/note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
FT		and HLA-B35"
FT	Peptide	82. .91
FT		/note= "Peptide presented by MHC Class I HLA-A1"
FT	Peptide	82. .90
FT		/note= "Peptide presented by MHC Class I HLA-A1"
FT	Peptide	83. .91
FT		/note= "Peptide presented by MHC Class I HLA-B44"
FT	Peptide	84. .92
FT		/note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
FT		and HLA-B35"
FT	Peptide	87. .96
FT		/note= "Peptide presented by MHC Class I HLA-A1"
FT	Peptide	88. .96
FT		/note= "Peptide presented by MHC Class I HLA-B44"
FT	Peptide	96. .104
FT		/note= "Peptide presented by MHC Class I HLA-B7"
FT	Peptide	100. .108
FT		/note= "Peptide presented by MHC Class I HLA-B44"
FT	Peptide	102. .110
FT		/note= "Peptide presented by MHC Class I HLA-B44"
FT	Peptide	107. .116
FT		/note= "Peptide presented by MHC Class I HLA-A24"
FT	Peptide	110. .118
FT		/note= "Peptide presented by MHC Class I HLA-B52"
FT	Peptide	113. .122
FT		/note= "Peptide presented by MHC Class I HLA-B7 and HLA-
FT		B52"
FT	Peptide	113. .121
FT		/note= "Peptide presented by MHC Class I HLA-B7"
FT	Peptide	115. .124
FT		/note= "Peptide presented by MHC Class I HLA-A3"
FT	Peptide	118. .126
FT		/note= "Peptide presented by MHC Class I HLA-B35"
FT	Peptide	124. .133
FT		/note= "Peptide presented by MHC Class I HLA-B52"
FT	Peptide	125. .133
FT		/note= "Peptide presented by MHC Class I HLA-A24"
FT	Peptide	138. .147
FT		/note= "Peptide presented by MHC Class I HLA-B8"
FT	Peptide	139. .147
FT		/note= "Peptide presented by MHC Class I HLA-B7"
FT	Peptide	145. .153
FT		/note= "Peptide presented by MHC Class I HLA-A24 and HLA-
FT		B52"
FT	Peptide	153. .162
FT		/note= "Peptide presented by MHC Class I HLA-B52"
FT	Peptide	154. .163
FT		/note= "Peptide presented by MHC Class I HLA-B52"
FT	Peptide	154. .162
FT		/note= "Peptide presented by MHC Class I HLA-B52"
FT	Peptide	156. .167
FT		/note= "Peptide (AAY52434) presented by MHC Class I HLA-
FT		A2"
FT	Peptide	158. .166
FT		/note= "Peptide presented by MHC Class I HLA-A3"

```
FT   Peptide          159. .167
FT                    /note= "Peptide presented by MHC Class I HLA-A3"
FT   Peptide          162. .170
FT                    /note= "Peptide presented by MHC Class I HLA-B52"
XX
PN   WO9953938-A1.
XX
PD   28-OCT-1999.
XX
PF   24-MAR-1999;   99WO-US006875.
XX
PR   17-APR-1998;   98US-00062422.
PR   02-OCT-1998;   98US-00165546.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Stockert E,  Jager E,  Chen Y,  Scanlan M,  Alexander K,  Old LJ;
PI   Gure A,  Ritter G;
XX
DR   WPI; 2000-038483/03.
DR   N-PSDB; AAZ38380.
XX
PT   Novel peptides which bind to MHC class I and MHC class II molecules,
PT   useful for therapeutic and diagnostic purposes.
XX
PS   Claim 30; Fig 3; 49pp; English.
XX
CC   This sequence represents a human tumour antigen, NY-ESO-1, the cDNA
CC   encoding which was isolated from an oesophagus squamous cell cancer cDNA
CC   library. Tissue localisation studies revealed it to be expressed at high
CC   levels in normal ovary and testis but not in normal colon, kidney, liver,
CC   brain, oesophagus and skin. It was expressed in certain tumours and
CC   tumour cell lines with some degree of frequency - these included melanoma
CC   specimens and cell lines, and breast and bladder cancer specimens, with
CC   expression in other tumour types being sporadic. Peptides derived from NY
CC   -ESO-1 are bound by both MHC (major histocompatibility complex) Class I
CC   and Class II molecules for presentation to T-cells. Peptides AAY52431-
CC   Y52434 bind to Class I HLA-A2 molecules, thereby stimulating
CC   proliferation of cytotoxic T-cells, while peptides AAY52435-Y52440 bind
CC   to Class II HLA-DR53 molecules, stimulating helper T-cell proliferation.
CC   The peptides derived from NY-ESO-1 may be used in methods and
CC   compositions used for the treatment, diagnosis and prevention of cancers
CC   (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma,
CC   ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to
CC   stimulate the proliferation of T cells
CC
CC   Revised record issued on 21-OCT-2004 : Correction to feature table key
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 64;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.51;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 12
AAY70862
ID   AAY70862 standard; protein; 180 AA.
XX
AC   AAY70862;
XX
DT   31-JUL-2000  (first entry)
XX
DE   Human tumour antigen, NY-ESO-1 protein.
XX
KW   NY-ESO-1; CAMEL; CTL-recognised Antigen on MELanoma; human; cancer; CTL;
KW   cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer;
KW   melanoma; immunotherapy; immune response.
XX
OS   Homo sapiens.
XX
PN   WO200023584-A1.
XX
PD   27-APR-2000.
XX
PF   15-OCT-1999;   99WO-EP007832.
XX
PR   16-OCT-1998;   98EP-00119583.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA   (UYHO-) UNIV HOSPITAL LEIDEN.
XX
PI   Schrier PI,  Aarnoudse CA,  Heider K,  Klade C;
XX
DR   WPI; 2000-339685/29.
DR   N-PSDB; AAD00152.
XX
PT   Tumor-associated antigen useful for cancer immunotherapy is encoded by
PT   the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
XX
PS   Example 3; Page 62-63; 73pp; English.
XX
CC   The present sequence is the human NY-ESO-1 protein, a tumour antigen,
CC   identified by screening an esophagus carcinoma cDNA library. This protein
CC   is derived from open reading frame (ORF)-1 that contain epitopes of
CC   tumour specific T-cells. NY-ESO-1 is expressed in different tumour types,
CC   but not in healthy tissues except in testis. It also shows homology with
CC   the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELanoma)
CC   protein, a tumour-asociated antigen. The tumour-associated antigen
CC   displayed on melanoma cells is recognised by cytotoxic T lymphocytes.
CC   This sequence has anticancer activity. CAMEL tumour antigen and
CC   immunogenic peptides derived from it are useful for cancer immunotherapy.
CC   They have the potential to induce an immune response, by eliciting a CTL
CC   response. The DNA molecule is used for the construction of recombinant or
CC   fusion proteins
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 64;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.51;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 13
AAB03154
ID   AAB03154 standard; protein; 180 AA.
XX
AC   AAB03154;
XX
DT   23-OCT-2000  (first entry)
XX
DE   Human oesophageal cancer-associated antigen NY-ESO-1.
XX
KW   Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen;
KW   oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain;
KW   antibody; diagnostic marker; drug delivery target.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   7
FT                    /note= "Potential N-myristoylation site"
FT   Modified-site   9
FT                    /note= "Potential N-myristoylation site"
FT   Modified-site   11
FT                    /note= "Potential O-phosphorylation site"
FT   Modified-site   98
FT                    /note= "Potential O-phosphorylation site"
```

```
FT   Modified-site   134
FT                   /note= "Potential O-phosphorylation site"
FT   Modified-site   138
FT                   /note= "Potential O-phosphorylation site"
FT   Domain          152. .172
FT                   /note= "Potential transmembrane domain"
XX
PN   US6069233-A.
XX
PD   30-MAY-2000.
XX
PF   26-JAN-1998;   98US-00013150.
XX
PR   03-OCT-1996;   96US-00725381.
XX
PA   (SLOK ) SLOAN KETTERING INST CANCER RES.
PA   (CORR ) CORNELL RES FOUND INC.
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Scanlan M,  Gure AO,  Chen Y,  Tureci O,  Sahin U,  Pfreundschuh M;
PI   Old LJ;
XX
DR   WPI; 2000-410880/35.
DR   N-PSDB; AAA61483.
XX
PT   New isolated esophageal cancer-associated antigen useful as markers for
PT   producing antibodies and as targets for identifying abnormal conditions,
PT   e.g. infections and cancer.
XX
PS   Example 5; Fig 3; 9pp; English.
XX
CC   This sequence represents a human oesophageal cancer-associated antigen,
CC   NY-ESO-1. The cDNA encoding this sequence was isolated from a cDNA
CC   library prepared from a specimen of well-to-moderately differentiated
CC   squamous cell cancer of the oesophagus. Expression analysis demonstrated
CC   that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma
CC   cell lines and in normal ovary and testis tissue, but not in normal
CC   colon, kidney, liver or brain tissue. Analysis of the amino acid sequence
CC   of the protein indicates that the protein has a transmembrane domain,
CC   several N-myristoylation sites and O-phosphorylation sites and that it
CC   contains antigenic sequences in the N-terminal half of the protein. The
CC   antigen is useful as an immunogen when combined with an adjuvant, in both
CC   precursor and post- translationally modified forms, and may be used to
CC   generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic
CC   marker for oesophageal cancer, and can be utilised as a marker for the
CC   targetted delivery of therapeutic agents to oesophageal cancer cells. It
CC   can also be used to generate diagnostic or therapeutic agents
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 64;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.51;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 14
AAB69946
ID   AAB69946 standard; protein; 180 AA.
XX
AC   AAB69946;
XX
DT   27-APR-2001  (first entry)
XX
DE   Human NY-ESO-1 protein.
XX
KW   Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW   HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW   non-small cell lung carcinoma; tumour status determination.
XX
OS   Homo sapiens.
XX
PN   WO200107917-A1.
XX
PD   01-FEB-2001.
XX
PF   14-JUL-2000; 2000WO-US019220.
XX
PR   23-JUL-1999;   99US-00359503.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (SLOK ) SLOAN KETTERING INST CANCER RES.
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Jager E,  Stockert E,  Old LJ,  Knuth A,  Chen Y,  Scanlan M;
XX
DR   WPI; 2001-182822/18.
DR   N-PSDB; AAF58634.
XX
PT   Method useful for determining the status (e.g. progression, regression or
PT   stability of the disease) of a cancerous condition, involves determining
PT   the levels of NY-ESO-1 specific antibodies in a sample taken from a
PT   patient.
XX
PS   Example 5; Fig 3; 50pp; English.
XX
CC   The present sequence is human NY-ESO-1 protein. It is provided in a
CC   specification relating to a method for determining the status of a
CC   cancerous condition in a patient with a tumour that expresses NY-ESO-1.
CC   The method comprises assaying a sample taken from the patient for
CC   antibodies that specifically bind to the NY-ESO-1 and comparing the value
CC   obtained to a prior value obtained from assay of a prior sample taken
CC   from the patient. Any difference between the values is indicative of a
CC   change in status of the cancerous condition. The method is useful for
CC   determining whether a cancerous condition is progressing, regressing or
CC   remaining stable, in particular in patients receiving treatment for a
CC   melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
CC   carcinoma
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 64;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.51;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 15
AAG67164
ID   AAG67164 standard; protein; 180 AA.
XX
AC   AAG67164;
XX
DT   13-NOV-2001  (first entry)
XX
DE   Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
XX
KW   Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW   HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
KW   cancer; testis tumour.
XX
OS   Homo sapiens.
XX
PN   WO200162917-A1.
XX
PD   30-AUG-2001.
XX
PF   22-JAN-2001; 2001WO-US002126.
XX
PR   22-FEB-2000; 2000US-00510635.
```

XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Lethe B, Boon-Falleur T;
XX
DR WPI; 2001-550091/61.
DR N-PSDB; AAH75118.
XX
PT Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful
PT for diagnosing testicular tumors.
XX
PS Example 5; Fig 3; 50pp; English.
XX
CC The present sequence represents cancer testis tumour antigen NY-ESO-1
CC (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
CC least one human leukocyte antigen (HLA) binding peptide, which binds to
CC Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is
CC expressed in tumour mRNA and in testis, but not normal colon, kidney,
CC liver or brain tissue. The presence or level of expression of NY-ESO-1
CC may be assayed for the diagnosis of cancer, especially testis tumours
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 64; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62
```

Search completed: March 13, 2006, 19:03:59
Job time : 90.3529 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:04:24 ; Search time 14.2588 Seconds
(without alignments)
80.975 Million cell updates/sec

Title: US-09-529-206E-29
Perfect score: 64
Sequence: 1 ARASGPGGGAPR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	44	68.8	3190	2	T13828	CREB-binding prote
2	42	65.6	185	2	T36874	hypothetical prote
3	42	65.6	201	2	G72663	hypothetical prote
4	42	65.6	222	2	T36115	probable oxidoredu
5	42	65.6	327	2	T29031	hypothetical prote
6	42	65.6	351	2	S50754	hypothetical prote
7	42	65.6	378	2	C87425	aldose 1-epimerase
8	42	65.6	436	2	T36104	conserved hypothet
9	42	65.6	474	2	G75580	conserved hypothet
10	41	64.1	173	2	AB3648	flagellar basal-bo
11	41	64.1	286	2	S04673	H+-transporting tw
12	41	64.1	357	2	F82878	XAA-PRO aminopepti
13	41	64.1	371	2	T39312	hypothetical prote
14	41	64.1	505	2	S68518	tub protein, brain
15	41	64.1	521	2	A29345	steroid hormone re
16	41	64.1	1207	2	T00378	KIAA0641 protein -
17	41	64.1	1690	2	T35694	ATP dependent DNA
18	40	62.5	82	2	T04476	acclimation protei
19	40	62.5	290	2	T36712	hypothetical prote
20	40	62.5	335	2	S08341	myristylated alani
21	40	62.5	379	1	A48082	MAP kinase 3 (EC 2
22	40	62.5	383	2	A86182	hypothetical prote
23	40	62.5	679	2	S02165	regulatory protein
24	40	62.5	910	2	A34721	androgen receptor
25	40	62.5	911	2	B34721	androgen receptor
26	40	62.5	919	2	A39248	androgen receptor
27	40	62.5	954	2	A87431	regulatory protein
28	39.5	61.7	730	2	A36226	collagen alpha 1 c
29	39	60.9	103	2	C72683	hypothetical prote
30	39	60.9	114	2	B45036	Pur beta - human (
31	39	60.9	163	2	E87464	competence/damage-
32	39	60.9	166	2	I69006	histocompatibility
33	39	60.9	187	2	T35619	hypothetical prote
34	39	60.9	197	2	S25825	polygalacturonase
35	39	60.9	213	2	S42585	DNA-invertase - Rh
36	39	60.9	260	2	F95899	probable transcrip
37	39	60.9	269	2	A47008	transcription acti
38	39	60.9	306	2	S25824	polygalacturonase
39	39	60.9	307	2	B72677	hypothetical prote
40	39	60.9	349	2	S55626	hypothetical prote
41	39	60.9	377	2	S28184	Ca2+/calmodulin-de
42	39	60.9	380	2	JC1451	Ca2+/calmodulin-de
43	39	60.9	387	2	T52451	endopeptidase Clp
44	39	60.9	410	2	S30067	polygalacturonase
45	39	60.9	410	2	S30066	polygalacturonase

ALIGNMENTS

RESULT 1
T13828
CREB-binding protein homolog - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13828
R;Akimaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; G
Nature 386, 735-738, 1997
A;Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling
A;Reference number: Z17785; MUID:97263578; PMID:9109493
A;Accession: T13828
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3190 <AKI>
A;Cross-references: UNIPROT:O01368; UNIPARC:UPI000003EB83; EMBL:U88570; NID:g1916929; P
C;Genetics:
A;Cross-references: FlyBase:FBgn0015624
A;Map position: X
F;1723-1780/Domain: bromodomain homology <BRO>

Query Match 68.8%; Score 44; DB 2; Length 3190;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SGPGGGAPR 12
:||||| ||
Db 320 NGPGGGGPR 328

RESULT 2
T36874
hypothetical protein SCI51.11c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36874
R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21617
A;Accession: T36874
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-185 <MUR>
A;Cross-references: UNIPROT:Q9S229; UNIPARC:UPI00000DB31A; EMBL:AL109848; PIDN:CAB52835
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCI51.11c

Query Match 65.6%; Score 42; DB 2; Length 185;
Best Local Similarity 80.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARASGPGGGA 10

```
              || |||| ||
Db         86 ARGSGPGSGA 95
```

RESULT 3
G72663
hypothetical protein APE0734 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72663
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: G72663
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-201 <KAW>
A;Cross-references: UNIPROT:Q9YE35; UNIPARC:UPI000005DC7C; DDBJ:AP000060; NID:g5104188;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0734
C;Superfamily: Aeropyrum pernix hypothetical protein APE0734

  Query Match 65.6%; Score 42; DB 2; Length 201;
  Best Local Similarity 75.0%; Pred. No. 54;
  Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 ARASGPGGGAPR 12
              ||||| ||  ||
Db         37 ARASGVGGRRPR 48
```

RESULT 4
T36115
probable oxidoreductase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C;Accession: T36115
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1999
A;Reference number: Z21597
A;Accession: T36115
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-222 <MUR>
A;Cross-references: UNIPROT:Q9X887; UNIPARC:UPI00000DB008; EMBL:AL049707; PIDN:CAB41281.
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCE15.12c
C;Superfamily: NAD(P)H-dependent FMN reductase (sulfate starvation-induced protein 4); S

  Query Match 65.6%; Score 42; DB 2; Length 222;
  Best Local Similarity 72.7%; Pred. No. 59;
  Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 ARASGPGGGAP 11
              ||||||  | |
Db        183 ARASGPSAGRP 193
```

RESULT 5
T29031
hypothetical protein F53G12.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29031
R;Wu, X.; Graves, T.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F53G12.
A;Reference number: Z20555
A;Accession: T29031
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-327 <WUX>
A;Cross-references: UNIPROT:O01799; UNIPARC:UPI0000078FFF; EMBL:AF003139; PIDN:AAB54156.
A;Experimental source: strain Bristol N2; clone F53G12
C;Genetics:
A;Gene: CESP:F53G12.7
A;Map position: 1
A;Introns: 59/3; 138/1; 223/2

  Query Match 65.6%; Score 42; DB 2; Length 327;
  Best Local Similarity 72.7%; Pred. No. 81;
  Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 ARASGPGGGAP 11
              | |:| |||||
Db        113 AEAAGGGGGAP 123
```

RESULT 6
S50754
hypothetical protein WP6 - Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S50754
R;Woessner, J.P.; Molendijk, A.J.; van Egmond, P.; Klis, F.M.; Goodenough, U.W.; Haring,
Plant Mol. Biol. 26, 947-960, 1994
A;Title: Domain conservation in several volvocalean cell wall proteins.
A;Reference number: S50754; MUID:95093034; PMID:8000007
A;Accession: S50754
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-351 <WOE>
A;Cross-references: UNIPROT:Q39492; UNIPARC:UPI00000A170A; EMBL:L29028; NID:g530877; PID

  Query Match 65.6%; Score 42; DB 2; Length 351;
  Best Local Similarity 80.0%; Pred. No. 86;
  Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 RASGPGGGAP 11
              ||| |||| |
Db        299 RASPPGGGPP 308
```

RESULT 7
C87425
aldose 1-epimerase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: C87425
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87425
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-378 <STO>
A;Cross-references: UNIPROT:Q9A8D6; UNIPARC:UPI00000C73A0; GB:AE005673; NID:g13422779; P
C;Genetics:
A;Gene: CC1418
C;Superfamily: aldose 1-epimerase

  Query Match 65.6%; Score 42; DB 2; Length 378;
  Best Local Similarity 77.8%; Pred. No. 91;
  Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          4 SGPGGGAPR 12
              :|| |||||
Db        282 NGPSGGAPR 290
```

```
RESULT 8
T36104
conserved hypothetical protein SCE15.01 - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36104
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1999
A;Reference number: Z21597
A;Accession: T36104
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-436 <MUR>
A;Cross-references: UNIPROT:Q8CJX1; UNIPARC:UPI000017AD99; EMBL:AL049707; PIDN:CAB41270.
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCE15.01

  Query Match             65.6%;  Score 42;  DB 2;  Length 436;
  Best Local Similarity   72.7%;  Pred. No. 1e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAP 11
              | ||||||  |
Db        151 ADASGPGGNTP 161


RESULT 9
G75580
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: G75580
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75580
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-474 <WHI>
A;Cross-references: UNIPROT:Q9RYN8; UNIPARC:UPI00000C166F; GB:AE001863; GB:AE001825; NID
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRA0272
A;Map position: 2
C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF0821

  Query Match             65.6%;  Score 42;  DB 2;  Length 474;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGA 10
              | | ||||||
Db        319 ATAGGPGGGA 328


RESULT 10
AB3648
flagellar basal-body rod protein flgF [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AB3648
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AB3648
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <KUR>
A;Cross-references: UNIPROT:Q8YAZ4; UNIPARC:UPI0000058740; GB:AE008918; PIDN:AAL54349.1
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII1107
A;Map position: II

  Query Match             64.1%;  Score 41;  DB 2;  Length 173;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 PGGGAPR 12
              |||||||
Db        132 PGGGAPR 138


RESULT 11
S04673
H+-transporting two-sector ATPase (EC 3.6.3.14) gamma chain - Rhodopseudomonas blastica
C;Species: Rhodopseudomonas blastica
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 31-Dec-2004
C;Accession: S04673
R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A;Title: Rhodopseudomonas blastica atp operon. Nucleotide sequence and transcription.
A;Reference number: S04666; MUID:85058188; PMID:6209404
A;Accession: S04673
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-286 <TYB>
A;Cross-references: UNIPROT:P05436; UNIPARC:UPI0000126582
C;Superfamily: H(+)-transporting ATP synthase gamma chain
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

  Query Match             64.1%;  Score 41;  DB 2;  Length 286;
  Best Local Similarity   80.0%;  Pred. No. 99;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 ASGPGGGAPR 12
              ||| | ||||
Db         57 ASGQGAGAPR 66


RESULT 12
F82878
XAA-PRO aminopeptidase UU532 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: F82878
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mi
A;Reference number: A82870
A;Accession: F82878
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <GLA>
A;Cross-references: UNIPARC:UPI00000C1CAC; GB:AE002152; GB:AF222894; NID:g6899532; PIDN
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: pepP; UU532
A;Genetic code: SGC3
C;Superfamily: X-Pro aminopeptidase

  Query Match             64.1%;  Score 41;  DB 2;  Length 357;
  Best Local Similarity   77.8%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 ASGPGGGAP 11
              |||| ||:|
Db        193 ASGPNGGSP 201
```

RESULT 13
T39312
hypothetical protein SPBC119.14 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39312
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, March 1998
A;Reference number: Z21843
A;Accession: T39312
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-371 <WOO>
A;Cross-references: UNIPROT:O42905; UNIPARC:UPI00001352D5; EMBL:AL022117; PIDN:CAA17929.
A;Experimental source: strain 972h-; cosmid c119
C;Genetics:
A;Gene: SPDB:SPBC119.14
A;Map position: 2
A;Introns: 77/3; 105/3; 165/3; 250/1; 276/2

  Query Match 64.1%; Score 41; DB 2; Length 371;
  Best Local Similarity 70.0%; Pred. No. 1.2e+02;
  Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARASGPGGGA 10
:| ||||||:
Db 35 SRRSGPGGGS 44

RESULT 14
S68518
tub protein, brain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Nov-1996 #sequence_revision 27-Feb-1997 #text_change 31-Dec-2004
C;Accession: S68518; S68519
R;Noben-Trauth, K.; Naggert, J.K.; North, M.A.; Nishina, P.M.
Nature 380, 534-538, 1996
A;Title: A candidate gene for the mouse mutation tubby.
A;Reference number: S68518; MUID:96195061; PMID:8606774
A;Accession: S68518
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-505 <NOB>
A;Cross-references: UNIPROT:P50586; UNIPARC:UPI000002367A; EMBL:U52433; NID:g1279765; PI
A;Accession: S68519
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 47-505 <NO2>
A;Cross-references: UNIPARC:UPI00001488EE; EMBL:U52824; NID:g1280436; PIDN:AAC52512.1; P
C;Superfamily: tubby

  Query Match 64.1%; Score 41; DB 2; Length 505;
  Best Local Similarity 75.0%; Pred. No. 1.6e+02;
  Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARASGPGGGAPR 12
| ||| |||||
Db 113 AAASGGQGGAPR 124

RESULT 15
A29345
steroid hormone receptor ERR1 precursor - human
N;Alternate names: estrogen-related receptor
C;Species: Homo sapiens (man)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 31-Dec-2004
C;Accession: A29345; A49074
R;Giguere, V.; Yang, N.; Segui, P.; Evans, R.M.
Nature 331, 91-94, 1988
A;Title: Identification of a new class of steroid hormone receptors.
A;Reference number: A29345; MUID:88122546; PMID:3267207
A;Accession: A29345
A;Molecule type: mRNA
A;Residues: 1-521 <GIG>
A;Cross-references: UNIPROT:P11474; UNIPARC:UPI0000142399; EMBL:X51416; NID:g36608; PIDN
R;Wiley, S.R.; Kraus, R.J.; Zuo, F.; Murray, E.E.; Loritz, K.; Mertz, J.E.
Genes Dev. 7, 2206-2219, 1993
A;Title: SV40 early-to-late switch involves titration of cellular transcriptional repres
A;Reference number: A49074; MUID:94040741; PMID:8224847
A;Accession: A49074
A;Status: preliminary
A;Molecule type: protein
A;Residues: 166-169,'X',171-173 <WIL>
A;Cross-references: UNIPARC:UPI000017A1DF
C;Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zi
F;174-434/Domain: erbA transforming protein homology <ERBA>
F;176-196/Region: zinc finger
F;212-236/Region: zinc finger

  Query Match 64.1%; Score 41; DB 2; Length 521;
  Best Local Similarity 66.7%; Pred. No. 1.6e+02;
  Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARASGPGGGAPR 12
| :|||||
Db 462 AGRAGPGGGAER 473

Search completed: March 13, 2006, 19:16:11
Job time : 14.2588 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 18:53:23 ; Search time 87.1059 Seconds
(without alignments)
97.196 Million cell updates/sec

Title: US-09-529-206E-29
Perfect score: 64
Sequence: 1 ARASGPGGGAPR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	64	100.0	142	2	Q9NY13_HUMAN	Q9ny13 homo sapien
2	64	100.0	180	1	CTG1B_HUMAN	P78358 homo sapien
3	64	100.0	180	2	Q7LBY4_HUMAN	Q7lby4 homo sapien
4	56	87.5	210	1	CTAG2_HUMAN	O75638 homo sapien
5	54	84.4	362	2	Q63QT8_BURPS	Q63qt8 burkholderi
6	54	84.4	362	2	Q62H22_BURMA	Q62h22 burkholderi
7	50	78.1	194	2	Q96BU2_HUMAN	Q96bu2 homo sapien
8	50	78.1	896	2	Q96D18_HUMAN	Q96d18 homo sapien
9	50	78.1	1253	2	Q6DHV6_HUMAN	Q6dhv6 homo sapien
10	50	78.1	1430	2	Q9H7P9_HUMAN	Q9h7p9 homo sapien
11	48	75.0	262	2	Q5Z8E2_ORYSA	Q5z8e2 oryza sativ
12	48	75.0	321	2	Q96S27_HUMAN	Q96s27 homo sapien
13	48	75.0	449	2	Q7F1E3_ORYSA	Q7f1e3 oryza sativ
14	47	73.4	367	2	Q6AV33_ORYSA	Q6av33 oryza sativ
15	47	73.4	895	2	Q4NUK4_9DELT	Q4nuk4 anaeromyxob
16	46	71.9	175	1	PACA_CHICK	P41534 g glucagon-
17	46	71.9	327	2	Q63HT9_BURPS	Q63ht9 burkholderi
18	46	71.9	330	2	Q629N3_BURMA	Q629n3 burkholderi
19	46	71.9	383	2	Q4TEG9_TETNG	Q4teg9 tetraodon n
20	46	71.9	695	2	Q4T320_TETNG	Q4t320 tetraodon n
21	46	71.9	708	2	Q5KJM5_CRYNE	Q5kjm5 cryptococcu
22	46	71.9	708	2	Q55WM1_CRYNE	Q55wm1 cryptococcu
23	46	71.9	788	2	Q4QQP8_HUMAN	Q4qqp8 homo sapien
24	46	71.9	1000	2	Q4FKF7_9TRYP	Q4fkf7 trypanosoma
25	45	70.3	309	2	Q63N33_BURPS	Q63n33 burkholderi
26	45	70.3	322	2	Q67PJ0_SYMTH	Q67pj0 symbiobacte
27	45	70.3	337	1	CT086_HUMAN	Q9bz19 homo sapien
28	45	70.3	432	2	Q7L0R7_HUMAN	Q7l0r7 homo sapien
29	45	70.3	444	2	Q9UPQ2_HUMAN	Q9upq2 homo sapien
30	45	70.3	472	2	Q51LM2_MAGGR	Q51lm2 magnaporthe
31	45	70.3	504	2	Q4NVJ7_9DELT	Q4nvj7 anaeromyxob
32	45	70.3	559	2	Q8L680_ORYSA	Q8l680 oryza sativ
33	45	70.3	678	2	Q8NAC4_HUMAN	Q8nac4 homo sapien
34	45	70.3	730	2	Q4NZ61_9DELT	Q4nz61 anaeromyxob
35	45	70.3	867	2	Q94LD1_ORYSA	Q94ld1 oryza sativ
36	45	70.3	905	2	Q4NTZ7_9DELT	Q4ntz7 anaeromyxob
37	45	70.3	1379	2	Q7QEK5_ANOGA	Q7qek5 anopheles g
38	45	70.3	1383	2	Q4SW43_TETNG	Q4sw43 tetraodon n
39	45	70.3	2013	2	Q4NWX4_9DELT	Q4nwx4 anaeromyxob
40	44	68.8	111	2	Q5NTA5_CANFA	Q5nta5 canis famil
41	44	68.8	159	2	Q63KC9_BURPS	Q63kc9 burkholderi
42	44	68.8	159	2	Q62DA7_BURMA	Q62da7 burkholderi
43	44	68.8	159	2	Q4RBL9_TETNG	Q4rbl9 tetraodon n
44	44	68.8	162	2	Q6YUN8_ORYSA	Q6yun8 oryza sativ
45	44	68.8	163	2	Q6AD35_LEIXX	Q6ad35 leifsonia x

ALIGNMENTS

RESULT 1
Q9NY13_HUMAN
ID Q9NY13_HUMAN PRELIMINARY; PRT; 142 AA.
AC Q9NY13;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein LAGE-2 (Fragment).
GN Name=LAGE-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ275978; CAB76945.1; -; mRNA.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;

Query Match 100.0%; Score 64; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARASGPGGGAPR 12
||||||||||||
Db 25 ARASGPGGGAPR 36

RESULT 2
CTG1B_HUMAN
ID CTG1B_HUMAN STANDARD; PRT; 180 AA.
AC P78358;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-
DE ESO-1).
GN Name=CTAG1B; Synonyms=CTAG, CTAG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
RA Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,
RA Williamson B., Stockert E., Pfreundschuh M., Old L.J.;
RT "A testicular antigen aberrantly expressed in human cancers detected
RT by autologous antibody screening.";

```
RL   Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Melanoma;
RX   MEDLINE=98289662; PubMed=9626360;
RA   Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA   de Plaen E., Boon T.;
RT   "LAGE-1, a new gene with tumor specificity.";
RL   Int. J. Cancer 76:903-908(1998).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98430682; PubMed=9759882;
RA   Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,
RA   Schwartzentruber D.J., Rosenberg S.A.;
RT   "A breast and melanoma-shared tumor antigen: T cell responses to
RT   antigenic peptides translated from different open reading frames.";
RL   J. Immunol. 161:3596-3606(1998).
CC   -!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide
CC       variety of cancers. Detected in uterine myometrium.
CC   -!- SIMILARITY: Belongs to the CTAG family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U87459; AAB49693.1; -; mRNA.
DR   EMBL; AJ003149; CAA05908.1; -; mRNA.
DR   EMBL; AF038567; AAD05202.1; -; mRNA.
DR   HGNC; HGNC:2491; CTAG1B.
DR   MIM; 300156; -.
KW   Antigen; Transmembrane.
FT   TRANSMEM    156    172       Potential.
FT   COMPBIAS      5     82       Gly-rich.
SQ   SEQUENCE   180 AA;  17992 MW;  B122C5C2C8BE1569 CRC64;

  Query Match             100.0%;  Score 64;  DB 1;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 3
Q7LBY4_HUMAN
ID   Q7LBY4_HUMAN PRELIMINARY;      PRT;   180 AA.
AC   Q7LBY4;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
DE   antigen 1-A).
GN   Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21303268;
RA   Galgoczy P., Rosenthal A., Platzer M.;
RT   "Human-mouse comparative sequence analysis of the NEMO gene reveals an
RT   alternative promoter within the neighboring G6PD gene.";
RL   Gene 271:93-98(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21566154; PubMed=11709543; DOI=10.1093/hmg/10.22.2557;
RA   Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
RA   Patlan H., Ciccodicola A., Kenwrick S., Platzer M., D'Urso M.,
RA   Nelson D.L.;
RT   "Multiple pathogenic and benign genomic rearrangements occur at a 35
RT   kb duplication involving the NEMO and LAGE2 genes.";
RL   Hum. Mol. Genet. 10:2557-2567(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Platzer M.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Platzer M.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RA   Galgoczy P., Platzer M.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99454989; PubMed=10523621;
RA   De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
RT   "DNA methylation is the primary silencing mechanism for a set of germ
RT   line- and tumor-specific genes with a CpG-rich promoter.";
RL   Mol. Cell. Biol. 19:7327-7335(1999).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RA   Lethe B.G.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF277315; AAL27014.1; -; Genomic_DNA.
DR   EMBL; AJ275977; CAB76943.1; -; Genomic_DNA.
DR   EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
SQ   SEQUENCE   180 AA;  17992 MW;  B122C5C2C8BE1569 CRC64;

  Query Match             100.0%;  Score 64;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 4
CTAG2_HUMAN
ID   CTAG2_HUMAN    STANDARD;      PRT;   210 AA.
AC   O75638; O75637; Q9BU80; Q9UJ89; Q9Y479;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
GN   Name=CTAG2; Synonyms=ESO2, LAGE1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B).
RC   TISSUE=Melanoma;
RX   MEDLINE=98289662; PubMed=9626360;
RA   Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA   de Plaen E., Boon T.;
RT   "LAGE-1, a new gene with tumor specificity.";
RL   Int. J. Cancer 76:903-908(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B), AND VARIANTS
RP   GLN-6; GLN-89 AND ARG-138.
RC   TISSUE=Melanoma;
RX   MEDLINE=99325550; PubMed=10399963;
RA   Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT   "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT   unexpected translation product of LAGE-1.";
RL   Int. J. Cancer 82:442-448(1999).
RN   [3]
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RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
RP   ARG-138.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=LAGE-1B; Synonyms=LAGE-1L;
CC         IsoId=O75638-1; Sequence=Displayed;
CC       Name=LAGE-1A; Synonyms=LAGE-1S;
CC         IsoId=O75638-2; Sequence=VSP_004301;
CC   -!- TISSUE SPECIFICITY: Testis and very low level in placenta and in
CC       some uterus samples. Observed in 25-50% of tumor samples of
CC       melanomas, non-small-cell lung carcinomas, bladder, prostate and
CC       head and neck cancers.
CC   -!- DOMAIN: A transmembrane domain is present in isoform LAGE-1A.
CC   -!- SIMILARITY: Belongs to the CTAG family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AJ223093; CAA11117.1; -; Genomic_DNA.
DR   EMBL; AJ223093; CAA11116.1; -; Genomic_DNA.
DR   EMBL; AJ223040; CAA11043.1; -; mRNA.
DR   EMBL; AJ223041; CAA11044.1; -; mRNA.
DR   EMBL; AJ012834; CAA10194.1; -; mRNA.
DR   EMBL; AJ012835; CAA10196.1; -; mRNA.
DR   EMBL; BC002833; AAH02833.1; -; mRNA.
DR   Ensembl; ENSG00000126890; Homo sapiens.
DR   HGNC; HGNC:2492; CTAG2.
DR   H-InvDB; HIX0017163; -.
DR   MIM; 300396; -.
KW   Alternative splicing; Antigen; Polymorphism; Transmembrane.
FT   COMPBIAS       5     79       Gly-rich.
FT   COMPBIAS     183    188       Poly-Pro.
FT   VARSPLIC     135    210       MSVWDQDREGAGRMRVVGWGLGSASPEGQKARDLRTPKHKV
FT                                 SEQRPGTPGPPPPEGAQGDGCRGVAFNVMFSAPHI -> IR
FT                                 LTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQAPSG
FT                                 QRR (in isoform LAGE-1A).
FT                                 /FTId=VSP_004301.
FT   VARIANT        6      6       R -> Q.
FT                                 /FTId=VAR_007855.
FT   VARIANT       89     89       E -> Q.
FT                                 /FTId=VAR_007856.
FT   VARIANT      138    138       W -> R.
FT                                 /FTId=VAR_007857.
SQ   SEQUENCE   210 AA;  21120 MW;  8BE0EE00AE55E8BE CRC64;

  Query Match             87.5%;  Score 56;  DB 1;  Length 210;
  Best Local Similarity   91.7%;  Pred. No. 2.8;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              |||||| |||||
Db         51 ARASGPRGGAPR 62


RESULT 5
Q63QT8_BURPS
ID   Q63QT8_BURPS PRELIMINARY;      PRT;   362 AA.
AC   Q63QT8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative DNA polymerase III.
GN   OrderedLocusNames=BPSL2936;
OS   Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia; pseudomallei group.
OX   NCBI_TaxID=28450;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=K96243;
RX   PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA   Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
RA   Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA   Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
RA   Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA   Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D.,
RA   Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA   Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA   Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA   Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA   Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT   "Genomic plasticity of the causative agent of melioidosis,
RT   Burkholderia pseudomallei.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR   EMBL; BX571965; CAH36946.1; -; Genomic_DNA.
DR   GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR   GO; GO:0006260; P:DNA replication; IEA.
DR   InterPro; IPR010372; DNA_pol3_delta.
DR   InterPro; IPR005790; DNA_polIII_delta.
DR   Pfam; PF06144; DNA_pol3_delta; 1.
DR   TIGRFAMs; TIGR01128; holA; 1.
KW   Complete proteome.
SQ   SEQUENCE   362 AA;  38726 MW;  D5FF3DE783D41E41 CRC64;

  Query Match             84.4%;  Score 54;  DB 2;  Length 362;
  Best Local Similarity   83.3%;  Pred. No. 9.3;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              |||:|||| |||
Db        348 ARAAGPGGDAPR 359


RESULT 6
Q62H22_BURMA
ID   Q62H22_BURMA PRELIMINARY;      PRT;   362 AA.
AC   Q62H22;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   DNA polymerase III, delta subunit (EC 2.7.7.7).
GN   Name=holA; OrderedLocusNames=BMA2451;
OS   Burkholderia mallei (Pseudomonas mallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia.
OX   NCBI_TaxID=13373;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ATCC 23344;
RX   PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA   Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
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RA   Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA   Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA   Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA   Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
RA   Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA   Zafar N., Zhou L., Fraser C.M.;
RT   "Structural flexibility in the Burkholderia mallei genome.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR   EMBL; CP000010; AAU49707.1; -; Genomic_DNA.
DR   TIGR; BMA2451; -.
DR   GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006260; P:DNA replication; IEA.
DR   InterPro; IPR010372; DNA_pol3_delta.
DR   InterPro; IPR005790; DNA_polIII_delta.
DR   Pfam; PF06144; DNA_pol3_delta; 1.
DR   TIGRFAMs; TIGR01128; holA; 1.
KW   Complete proteome; Nucleotidyltransferase; Transferase.
SQ   SEQUENCE   362 AA;  38726 MW;  D5FF3DE783D41E41 CRC64;

  Query Match             84.4%;  Score 54;  DB 2;  Length 362;
  Best Local Similarity   83.3%;  Pred. No. 9.3;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              |||:|||| |||
Db        348 ARAAGPGGDAPR 359


RESULT 7
Q96BU2_HUMAN
ID   Q96BU2_HUMAN PRELIMINARY;      PRT;   194 AA.
AC   Q96BU2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   PLEKHG2 protein (Fragment).
GN   Name=PLEKHG2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pancreas;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pancreas;
RA   Director MGC Project;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC015174; AAH15174.1; -; mRNA.
FT   NON_TER       1      1
SQ   SEQUENCE   194 AA;  19957 MW;  91AB4FF8F05CBD3C CRC64;

  Query Match             78.1%;  Score 50;  DB 2;  Length 194;
  Best Local Similarity   81.8%;  Pred. No. 19;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAP 11
              ||  |||||||
Db         99 ARRQGPGGGAP 109


RESULT 8
Q96D18_HUMAN
ID   Q96D18_HUMAN PRELIMINARY;      PRT;   896 AA.
AC   Q96D18;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PLEKHG2 protein.
GN   Name=PLEKHG2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pancreas;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pancreas;
RA   Director MGC Project;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013426; AAH13426.1; -; mRNA.
SQ   SEQUENCE   896 AA;  94247 MW;  0DE6869BCFD4C471 CRC64;

  Query Match             78.1%;  Score 50;  DB 2;  Length 896;
  Best Local Similarity   81.8%;  Pred. No. 84;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAP 11
              ||  |||||||
Db        801 ARRQGPGGGAP 811


RESULT 9
Q6DHV6_HUMAN
ID   Q6DHV6_HUMAN PRELIMINARY;      PRT;  1253 AA.
AC   Q6DHV6;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
```

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DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   PLEKHG2 protein (Fragment).
GN   Name=PLEKHG2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pancreas;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pancreas;
RA   Director MGC Project;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 PH domain.
DR   EMBL; BC075858; AAH75858.1; -; mRNA.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR000219; RhoGEF.
DR   Pfam; PF00169; PH; 1.
DR   Pfam; PF00621; RhoGEF; 1.
DR   SMART; SM00233; PH; 1.
DR   SMART; SM00325; RhoGEF; 1.
DR   PROSITE; PS50010; DH_2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   1253 AA;  134404 MW;  534EB31283E535C5 CRC64;

  Query Match             78.1%;  Score 50;  DB 2;  Length 1253;
  Best Local Similarity   81.8%;  Pred. No. 1.2e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAP 11
              ||  |||||||
Db       1158 ARRQGPGGGAP 1168


RESULT 10
Q9H7P9_HUMAN
ID   Q9H7P9_HUMAN PRELIMINARY;      PRT;  1430 AA.
AC   Q9H7P9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   FLJ00018 protein (Fragment).
GN   Name=PLEKHG2; Synonyms=FLJ00018;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   PubMed=14702039; DOI=10.1038/ng1285;
RA   Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA   Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA   Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA   Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA   Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA   Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA   Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA   Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA   Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA   Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA   Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA   Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA   Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA   Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA   Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA   Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA   Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA   Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA   Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
CC   -!- SIMILARITY: Contains 1 PH domain.
DR   EMBL; AK024429; BAB15719.1; -; mRNA.
DR   HSSP; Q64096; 1KZ7.
DR   Ensembl; ENSG00000090924; Homo sapiens.
DR   HGNC; HGNC:29515; PLEKHG2.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR000219; RhoGEF.
DR   Pfam; PF00169; PH; 1.
DR   Pfam; PF00621; RhoGEF; 1.
DR   SMART; SM00233; PH; 1.
DR   SMART; SM00325; RhoGEF; 1.
DR   PROSITE; PS50010; DH_2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   1430 AA;  152528 MW;  E4DF0BFDACCB6A30 CRC64;

  Query Match             78.1%;  Score 50;  DB 2;  Length 1430;
  Best Local Similarity   81.8%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAP 11
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Db       1335 ARRQGPGGGAP 1345


RESULT 11
Q5Z8E2_ORYSA
ID   Q5Z8E2_ORYSA PRELIMINARY;      PRT;   262 AA.
AC   Q5Z8E2;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein P0487E11.17.
GN   Name=P0487E11.17;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
```

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OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
RA   Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA   Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA   Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA   Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA   Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA   Ikeno M., Ito S., Ito T., Ito Y., Ito Y., Iwabuchi A., Kamiya K.,
RA   Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA   Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA   Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA   Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA   Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA   Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA   Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y.,
RA   Yano M., Jiang J., Gojobori T.;
RT   "The genome sequence and structure of rice chromosome 1.";
RL   Nature 420:312-316(2002).
DR   EMBL; AP003793; BAD53925.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   262 AA;  27141 MW;  816A1189E43BA42A CRC64;

  Query Match             75.0%;  Score 48;  DB 2;  Length 262;
  Best Local Similarity   83.3%;  Pred. No. 50;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||| |||| |
Db        225 ARASGDGGGADR 236


RESULT 12
Q96S27_HUMAN
ID   Q96S27_HUMAN PRELIMINARY;      PRT;   321 AA.
AC   Q96S27;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein gene X.
GN   Name=gene X;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21096910; PubMed=11157797; DOI=10.1093/hmg/10.4.339;
RA   Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA   Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA   Higgs D.R.;
RT   "Sequence, structure and pathology of the fully annotated terminal 2
RT   Mb of the short arm of human chromosome 16.";
RL   Hum. Mol. Genet. 10:339-352(2001).
DR   EMBL; AE006463; AAK61225.1; -; Genomic_DNA.
DR   Ensembl; ENSG00000167933; Homo sapiens.
KW   Hypothetical protein.
SQ   SEQUENCE   321 AA;  32979 MW;  9C8764CFA17F4CD4 CRC64;

  Query Match             75.0%;  Score 48;  DB 2;  Length 321;
  Best Local Similarity   75.0%;  Pred. No. 60;
  Matches    9;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              || :|||||| |
Db          6 ARRAGPGGGAAR 17


RESULT 13
Q7F1E3_ORYSA
ID   Q7F1E3_ORYSA PRELIMINARY;      PRT;   449 AA.
AC   Q7F1E3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Hypothetical protein OJ1191_A10.131 (Hypothetical protein
DE   OJ1014_E06.5).
GN   Name=OJ1191_A10.131; Synonyms=OJ1014_E06.5;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR   EMBL; AP003857; BAD08744.1; -; Genomic_DNA.
DR   EMBL; AP003888; BAD11573.1; -; Genomic_DNA.
DR   Gramene; Q7F1E3; -.
DR   GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0016567; P:protein ubiquitination; IEA.
DR   InterPro; IPR008700; NOI.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF05627; NOI; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ   SEQUENCE   449 AA;  47196 MW;  B8EFF7708B292296 CRC64;

  Query Match             75.0%;  Score 48;  DB 2;  Length 449;
  Best Local Similarity   75.0%;  Pred. No. 84;
  Matches    9;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              :|| | ||||||
Db        156 SRAKGGGGGAPR 167


RESULT 14
Q6AV33_ORYSA
ID   Q6AV33_ORYSA PRELIMINARY;      PRT;   367 AA.
AC   Q6AV33;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein OSJNBa0063J18.9.
GN   Name=OSJNBa0063J18.9;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA   Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA   Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA   Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA   Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA   White O., Salzberg S.L., Fraser C.M.;
RT   "Oryza sativa chromosome 3 BAC OSJNBa0063J18 genomic sequence.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Buell R.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC107206; AAT77052.1; -; Genomic_DNA.
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DR   Gramene; Q6AV33; -.
KW   Hypothetical protein.
SQ   SEQUENCE   367 AA;  37474 MW;  B8C62D9D4CC18C86 CRC64;

  Query Match             73.4%;  Score 47;  DB 2;  Length 367;
  Best Local Similarity   75.0%;  Pred. No. 96;
  Matches    9;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              | ||||||| : |
Db         92 AAASGPGGGSAR 103


RESULT 15
Q4NUK4_9DELT
ID   Q4NUK4_9DELT PRELIMINARY;      PRT;   895 AA.
AC   Q4NUK4;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   LigA.
GN   ORFNames=AdehDRAFT_2813;
OS   Anaeromyxobacter dehalogenans 2CP-C.
OC   Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC   Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
OX   NCBI_TaxID=290397;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=2CP-C;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome assembly of Anaeromyxobacter
RT   dehalogenans 2CP-C.";
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=2CP-C;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Anaeromyxobacter
RT   dehalogenans 2CP-C.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAHD01000013; EAL79351.1; -; Genomic_DNA.
SQ   SEQUENCE   895 AA;  93871 MW;  0AE25BBBF172BDB0 CRC64;

  Query Match             73.4%;  Score 47;  DB 2;  Length 895;
  Best Local Similarity   81.8%;  Pred. No. 2.3e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 RASGPGGGAPR 12
              || | ||||||
Db        799 RARGAGGGAPR 809


Search completed: March 13, 2006, 19:14:28
Job time : 88.1059 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:14:49 ; Search time 22.3059 Seconds
(without alignments)
44.477 Million cell updates/sec

Title: US-09-529-206E-29
Perfect score: 64
Sequence: 1 ARASGPGGGAPR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	64	100.0	180	1	US-08-791-495-9	Sequence 9, Appli
2	64	100.0	180	2	US-08-937-263B-8	Sequence 8, Appli
3	64	100.0	180	2	US-09-751-798-8	Sequence 8, Appli
4	64	100.0	180	2	US-09-392-714-25	Sequence 25, Appl
5	64	100.0	180	2	US-09-165-546D-15	Sequence 15, Appl
6	64	100.0	180	2	US-09-341-829A-9	Sequence 9, Appli
7	64	100.0	180	2	US-09-849-602-30	Sequence 30, Appl
8	56	87.5	180	1	US-08-791-495-7	Sequence 7, Appli
9	56	87.5	180	2	US-09-341-829A-7	Sequence 7, Appli
10	56	87.5	210	1	US-08-791-495-5	Sequence 5, Appli
11	56	87.5	210	2	US-09-341-829A-5	Sequence 5, Appli
12	48	75.0	9	2	US-09-344-040C-117	Sequence 117, App
13	48	75.0	9	2	US-09-833-039A-117	Sequence 117, App
14	48	75.0	809	2	US-09-252-991A-31759	Sequence 31759, A
15	46	71.9	143	2	US-08-789-329C-10	Sequence 10, Appl
16	46	71.9	160	2	US-09-252-991A-17249	Sequence 17249, A
17	46	71.9	172	2	US-08-789-329C-7	Sequence 7, Appli
18	46	71.9	175	2	US-08-789-329C-3	Sequence 3, Appli
19	46	71.9	210	2	US-09-252-991A-24923	Sequence 24923, A
20	45	70.3	416	2	US-09-252-991A-30219	Sequence 30219, A
21	45	70.3	421	2	US-09-252-991A-32326	Sequence 32326, A
22	45	70.3	678	2	US-10-104-047-3295	Sequence 3295, Ap
23	45	70.3	1427	2	US-09-252-991A-20577	Sequence 20577, A
24	44	68.8	196	2	US-09-252-991A-30527	Sequence 30527, A
25	44	68.8	456	2	US-09-252-991A-17335	Sequence 17335, A
26	44	68.8	679	2	US-09-252-991A-27111	Sequence 27111, A
27	43	67.2	324	2	US-09-902-540-11047	Sequence 11047, A
28	43	67.2	1228	2	US-09-252-991A-17764	Sequence 17764, A
29	42	65.6	163	2	US-09-252-991A-29111	Sequence 29111, A
30	42	65.6	283	2	US-09-252-991A-17831	Sequence 17831, A
31	42	65.6	505	1	US-08-660-765A-2	Sequence 2, Appli
32	42	65.6	789	2	US-09-252-991A-25611	Sequence 25611, A
33	42	65.6	836	2	US-09-491-356C-21	Sequence 21, Appl
34	41.5	64.8	268	2	US-09-252-991A-31279	Sequence 31279, A
35	41	64.1	177	2	US-09-252-991A-18782	Sequence 18782, A
36	41	64.1	187	2	US-09-252-991A-29442	Sequence 29442, A
37	41	64.1	224	2	US-09-252-991A-30723	Sequence 30723, A
38	41	64.1	310	2	US-09-252-991A-19986	Sequence 19986, A
39	41	64.1	340	2	US-09-949-002-562	Sequence 562, App
40	41	64.1	412	1	US-08-878-989-6	Sequence 6, Appli
41	41	64.1	412	2	US-09-272-796-6	Sequence 6, Appli
42	41	64.1	438	2	US-09-949-016-7812	Sequence 7812, Ap
43	41	64.1	459	1	US-08-630-592-2	Sequence 2, Appli
44	41	64.1	459	1	US-08-714-991-2	Sequence 2, Appli
45	41	64.1	459	2	US-09-032-365A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth , Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 64; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARASGPGGGAPR 12
||||||||||||
Db 51 ARASGPGGGAPR 62

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RESULT 2
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
;  GENERAL INFORMATION:
;    APPLICANT:  Chen, Yao-Tseng; Scanlan, Matthew;
;    APPLICANT:  Gure, Ali; Old, Lloyd J.; Jager, Elke;
;    APPLICANT:  Alexander, Knuth; Drijfhout, Jan W.
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULE
;    TITLE OF INVENTION:  ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
;    TITLE OF INVENTION:  ITSELF, AND USES THEREOF
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/937,263B
;      FILING DATE:  September 15, 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sinn, Eric, Patent Agent
;      REGISTRATION NUMBER:  40,177
;      REFERENCE/DOCKET NUMBER:  LUD 5466.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3000
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-937-263B-8

  Query Match             100.0%;  Score 64;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
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Db         51 ARASGPGGGAPR 62


RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
;  GENERAL INFORMATION:
;    APPLICANT:  Stockert, Elisabeth; Jager, Elke;
;    APPLICANT:  Chen, Yao-tseng; Scanlan, Matthew;
;    APPLICANT:  Knuth, Alexander; Old, Lloyd J.
;    TITLE OF INVENTION:  Antibodies Which Bind to NY-ESO-1 Cancer
;    TITLE OF INVENTION:  Associated Proteins, Uses Thereof,
;    TITLE OF INVENTION:  Truncated Forms of NY-ESO-1, and HLA
;    TITLE OF INVENTION:  Binding Peptides Derived Therefrom
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/751,798
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/062,422
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 6525177man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3168
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-09-751-798-8

  Query Match             100.0%;  Score 64;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
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Db         51 ARASGPGGGAPR 62


RESULT 4
US-09-392-714-25
; Sequence 25, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT: Gure, Ali O.
;  APPLICANT: Williamson, Barbara
;  APPLICANT: Chen, Yao-Tseng
;  APPLICANT: Old, Lloyd J.
;  TITLE OF INVENTION: Cancer Associated Antigens and Uses
;  TITLE OF INVENTION: Therefor
;  FILE REFERENCE: L0461/7062
;  CURRENT APPLICATION NUMBER: US/09/392,714A
;  CURRENT FILING DATE: 1999-09-09
;  EARLIER APPLICATION NUMBER: PCT/US98/14679
;  EARLIER FILING DATE: 1998-07-15
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-392-714-25

  Query Match             100.0%;  Score 64;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
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Db         51 ARASGPGGGAPR 62
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RESULT 5
US-09-165-546D-15
; Sequence 15, Application US/09165546D
; Patent No. 6723832
;   GENERAL INFORMATION:
;        APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
;                   Gure, Ali, Old, Lloyd, Ritter, Gerd
;        TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                            SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
;                            USES THEREOF
;        NUMBER OF SEQUENCES: 15
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FULBRIGHT & JAWORSKI LLP
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10158
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/165,546D
;             FILING DATE: 02-Oct-1998
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: April 17, 1998
;             APPLICATION NUMBER: 08/937,263
;             FILING DATE: September 15, 1997
;             APPLICATION NUMBER: US 08/725,182
;             FILING DATE: October 3, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, No. 6723832man D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3000
;             TELEFAX: (212) 318-3400
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 180 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15

  Query Match             100.0%;  Score 64;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 6
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-9

  Query Match             100.0%;  Score 64;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 7
US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT:  Old, Lloyd J.
;  APPLICANT:  Stockert, Elisabeth
;  APPLICANT:  Chen, Yao-Tseng
;  TITLE OF INVENTION: Colon Cancer Antigen Panel
;  FILE REFERENCE: L0461/7105(JRV)
;  CURRENT APPLICATION NUMBER: US/09/849,602
;  CURRENT FILING DATE:  2001-05-04
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-849-602-30

  Query Match             100.0%;  Score 64;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 8
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL-1 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-791-495-7

  Query Match             87.5%;  Score 56;  DB 1;  Length 180;
  Best Local Similarity   91.7%;  Pred. No. 2.3;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              |||||| |||||
Db         51 ARASGPRGGAPR 62


RESULT 9
US-09-341-829A-7
; Sequence 7, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-7

  Query Match             87.5%;  Score 56;  DB 2;  Length 180;
  Best Local Similarity   91.7%;  Pred. No. 2.3;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              |||||| |||||
Db         51 ARASGPRGGAPR 62


RESULT 10
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godélaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL-1 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  210 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-791-495-5

  Query Match             87.5%;  Score 56;  DB 1;  Length 210;
  Best Local Similarity   91.7%;  Pred. No. 2.7;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              |||||| |||||
Db         51 ARASGPRGGAPR 62


RESULT 11
US-09-341-829A-5
; Sequence 5, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-5

  Query Match             87.5%;  Score 56;  DB 2;  Length 210;
  Best Local Similarity   91.7%;  Pred. No. 2.7;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              |||||| |||||
Db         51 ARASGPRGGAPR 62


RESULT 12
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US-09-344-040C-117
; Sequence 117, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
;  APPLICANT: Tureci, Ozlem
;  APPLICANT:  Sahin, Ugur
;  APPLICANT:  Pfreundschuh, Michael
;  APPLICANT:  Ramensee, Hans Georg
;  APPLICANT:  Stevanovic, Stefan
;  TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
;  TITLE OF INVENTION:  Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
;  TITLE OF INVENTION:  Gene, and Uses Thereof
;  FILE REFERENCE: LUD 5556.1
;  CURRENT APPLICATION NUMBER: US/09/344,040C
;  CURRENT FILING DATE:  1999-06-25
;  PRIOR APPLICATION NUMBER: US 09/105,839
;  PRIOR FILING DATE: 1998-06-26
;  PRIOR APPLICATION NUMBER: US 08/851,130
;  PRIOR FILING DATE: 1997-05-05
;  NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 117
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-344-040C-117

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Qy          2 RASGPGGGA 10
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Db          1 RASGPGGGA 9


RESULT 13
US-09-833-039A-117
; Sequence 117, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
;  APPLICANT: Tureci, Ozlem
;  APPLICANT:  Sahin, Ugur
;  APPLICANT:  Pfreundschuh, Michael
;  TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
;  FILE REFERENCE: LUD 5622.1
;  CURRENT APPLICATION NUMBER: US/09/833,039A
;  CURRENT FILING DATE:  2001-04-12
;  PRIOR APPLICATION NUMBER: US 09/409,455
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: US 09/344,040
;  PRIOR FILING DATE: 1999-06-26
;  PRIOR APPLICATION NUMBER: US 09/105,839
;  PRIOR FILING DATE: 1998-06-26
;  NUMBER OF SEQ ID NOS: 131
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 117
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-833-039A-117

  Query Match             75.0%;  Score 48;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RASGPGGGA 10
              |||||||||
Db          1 RASGPGGGA 9


RESULT 14
US-09-252-991A-31759
; Sequence 31759, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 31759
;   LENGTH: 809
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31759

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Qy          2 RASGPGGGAPR 12
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Db        244 RAGGPRGGAPR 254


RESULT 15
US-08-789-329C-10
; Sequence 10, Application US/08789329C
; Patent No. 6165755
;  GENERAL INFORMATION:
;    APPLICANT:  SHERWOOD ET AL.
;    TITLE OF INVENTION:  CHICKEN NEUROPEPTIDE GENE USEFUL
;    TITLE OF INVENTION:  FOR IMPROVED POULTRY PRODUCTION
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klarquist Sparkman Campbell Leigh &
;      ADDRESSEE:  Whinston, LLP
;      STREET:  One World Trade Center
;      STREET:  121 S.W. Salmon Street
;      STREET:  Suite 1600
;      CITY:  Portland
;      STATE:  Oregon
;      COUNTRY:  United States of America
;      ZIP:  97204-2988
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Disk, 3-1/2 inch
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows NT
;      SOFTWARE:  WordPerfect 7.0 & ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/789,329C
;      FILING DATE:  01/23/97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Earp, David J.
;      REGISTRATION NUMBER:  41,401
;      REFERENCE/DOCKET NUMBER:  2847-46468/DJE
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (503) 226-7391
;      TELEFAX:  (503) 228-9446
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  143 aa
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-789-329C-10
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Query Match 71.9%; Score 46; DB 2; Length 143;
Best Local Similarity 72.7%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          2 RASGPGGGAPR 12
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Db         56 RAGAPGGGGPR 66
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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:51:56 ; Search time 72.5647 Seconds
(without alignments)
69.096 Million cell updates/sec

Title: US-09-529-206E-29
Perfect score: 64
Sequence: 1 ARASGPGGGAPR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	64	100.0	179	5	US-10-482-029-202	Sequence 202, App
3	64	100.0	180	3	US-09-751-798-8	Sequence 8, Appli
4	64	100.0	180	3	US-09-849-602-30	Sequence 30, Appl
5	64	100.0	180	4	US-10-023-182-8	Sequence 8, Appli
6	64	100.0	180	4	US-10-207-655-71	Sequence 71, Appl
7	64	100.0	180	4	US-10-364-614-14	Sequence 14, Appl
8	64	100.0	180	4	US-10-026-066-3	Sequence 3, Appli
9	64	100.0	180	4	US-10-117-937-74	Sequence 74, Appl
10	64	100.0	180	4	US-10-295-027-386	Sequence 386, App
11	64	100.0	180	4	US-10-296-734-832	Sequence 832, App
12	64	100.0	180	4	US-10-188-832-139	Sequence 139, App
13	64	100.0	180	4	US-10-777-053-11	Sequence 11, Appl
14	64	100.0	180	4	US-10-751-088-15	Sequence 15, Appl
15	64	100.0	180	4	US-10-657-022-74	Sequence 74, Appl
16	64	100.0	180	4	US-10-837-217-11	Sequence 11, Appl
17	64	100.0	180	5	US-10-877-373-9	Sequence 9, Appli
18	64	100.0	180	5	US-10-723-860-1270	Sequence 1270, Ap
19	64	100.0	180	5	US-10-871-708-7	Sequence 7, Appli
20	64	100.0	180	5	US-10-895-523-3	Sequence 3, Appli
21	64	100.0	180	5	US-10-182-506A-3	Sequence 3, Appli
22	64	100.0	180	5	US-10-756-149-5024	Sequence 5024, Ap
23	64	100.0	180	6	US-11-067-064-74	Sequence 74, Appl
24	64	100.0	180	6	US-11-067-159-74	Sequence 74, Appl
25	64	100.0	397	3	US-09-821-883-27	Sequence 27, Appl
26	64	100.0	397	6	US-11-144-912-27	Sequence 27, Appl
27	64	100.0	3541	4	US-10-296-734-1454	Sequence 1454, Ap
28	56	87.5	30	4	US-10-296-734-1436	Sequence 1436, Ap
29	56	87.5	135	4	US-10-295-027-388	Sequence 388, App
30	56	87.5	135	4	US-10-188-832-141	Sequence 141, App
31	56	87.5	180	4	US-10-146-473-69	Sequence 69, Appl
32	56	87.5	180	4	US-10-117-937-75	Sequence 75, Appl
33	56	87.5	180	4	US-10-296-734-834	Sequence 834, App
34	56	87.5	180	4	US-10-468-406-4	Sequence 4, Appli
35	56	87.5	180	4	US-10-657-022-75	Sequence 75, Appl
36	56	87.5	180	5	US-10-877-373-7	Sequence 7, Appli
37	56	87.5	180	6	US-11-067-064-75	Sequence 75, Appl
38	56	87.5	180	6	US-11-067-159-75	Sequence 75, Appl
39	56	87.5	210	4	US-10-157-031-88	Sequence 88, Appl
40	56	87.5	210	4	US-10-117-937-76	Sequence 76, Appl
41	56	87.5	210	4	US-10-657-022-76	Sequence 76, Appl
42	56	87.5	210	5	US-10-877-373-5	Sequence 5, Appli
43	56	87.5	210	6	US-11-067-064-76	Sequence 76, Appl
44	56	87.5	210	6	US-11-067-159-76	Sequence 76, Appl
45	55	85.9	10	4	US-10-447-161-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-10-296-734-1404
; Sequence 1404, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1404
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSO1a segment 4
US-10-296-734-1404

Query Match 100.0%; Score 64; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARASGPGGGAPR 12
||||||||||||
Db 8 ARASGPGGGAPR 19

RESULT 2
US-10-482-029-202
; Sequence 202, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-202

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  Query Match             100.0%;  Score 64;  DB 5;  Length 179;
  Best Local Similarity   100.0%;  Pred. No. 0.93;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. US20020010321A1
;  GENERAL INFORMATION:
;    APPLICANT:  Stockert, Elisabeth; Jager, Elke;
;    APPLICANT:  Chen, Yao-tseng; Scanlan, Matthew;
;    APPLICANT:  Knuth, Alexander; Old, Lloyd J.
;    TITLE OF INVENTION:  Antibodies Which Bind to NY-ESO-1 Cancer
;    TITLE OF INVENTION:  Associated Proteins, Uses Thereof,
;    TITLE OF INVENTION:  Truncated Forms of NY-ESO-1, and HLA
;    TITLE OF INVENTION:  Binding Peptides Derived Therefrom
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: 'Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/751,798
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/062,422
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. US20020010321A1man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3168
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-09-751-798-8

  Query Match             100.0%;  Score 64;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.94;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 4
US-09-849-602-30
; Sequence 30, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT:  Old, Lloyd J.
;  APPLICANT:  Stockert, Elisabeth
;  APPLICANT:  Chen, Yao-Tseng
;  TITLE OF INVENTION: Colon Cancer Antigen Panel
;  FILE REFERENCE: L0461/7105(JRV)
;  CURRENT APPLICATION NUMBER: US/09/849,602
;  CURRENT FILING DATE:  2001-05-04
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-849-602-30

  Query Match             100.0%;  Score 64;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.94;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 5
US-10-023-182-8
; Sequence 8, Application US/10023182
; Publication No. US20020164665A1
;  GENERAL INFORMATION:
;       APPLICANT: Stockert, Elisabeth; Jager, Elke;
;                  Chen, Yao-tseng; Scanlan, Matthew;
;                  Knuth, Alexander; Old, Lloyd J.
;       TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
;                           Associated Proteins, Uses Thereof,
;                           Truncated Forms of NY-ESO-1, and HLA
;                           Binding Peptides Derived Therefrom
;       NUMBER OF SEQUENCES: 8
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fulbright & Jaworski, L.L.P.
;            STREET: 666 Fifth Avenue
;            CITY: New York City
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10103
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;            COMPUTER: IBM
;            OPERATING SYSTEM: PC-DOS
;            SOFTWARE: WordPerfect
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/023,182
;            FILING DATE: 17-Dec-2001
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/751,798
;            FILING DATE: December 29, 2000
;            APPLICATION NUMBER: 09/062,422
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/725,182
;            FILING DATE: October 3, 1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Hanson, No. US20020164665A1man D.
;            REGISTRATION NUMBER: 30,946
;            REFERENCE/DOCKET NUMBER: LUD 5466.3
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 318-3168
;            TELEFAX: (212) 752-5958
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 180
;            TYPE: amino acid
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-023-182-8
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  Query Match             100.0%;  Score 64;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.94;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 6
US-10-207-655-71
; Sequence 71, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-207-655-71

  Query Match             100.0%;  Score 64;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.94;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 7
US-10-364-614-14
; Sequence 14, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
;  APPLICANT: JAGER, Elke
;  APPLICANT:  KNUTH, Alexander
;  APPLICANT:  OLD, Lloyd
;  APPLICANT:  Gnjatic, Sacha
;  TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
;  FILE REFERENCE: LUD 5726.1 CIP
;  CURRENT APPLICATION NUMBER: US/10/364,614
;  CURRENT FILING DATE:  2003-02-24
;  PRIOR APPLICATION NUMBER: US 60/355,828
;  PRIOR FILING DATE: 2002-02-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-364-614-14

  Query Match             100.0%;  Score 64;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.94;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 8
US-10-026-066-3
; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
; GENERAL INFORMATION:
;  APPLICANT: Simard, John J. L.
;  APPLICANT:  Diamond, David C.
;  TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
;  TITLE OF INVENTION:  PRESENTING CELLS
;  FILE REFERENCE: CTLIMM.21CP1C
;  CURRENT APPLICATION NUMBER: US/10/026,066
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: 09/561,074
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 09/560,465
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 09/561,572
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 09/561,571
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: PCT/US01/13806
;  PRIOR FILING DATE: 2001-04-27
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-026-066-3

  Query Match             100.0%;  Score 64;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.94;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 9
US-10-117-937-74
; Sequence 74, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
;  APPLICANT: CTL IMMUNO THERAPIES CORP.
;  APPLICANT:  SIMARD, John, J.L.
;  APPLICANT:  DIAMOND, David, C.
;  APPLICANT:  LIU, Liping
;  APPLICANT:  XIE, Zhidong
;  TITLE OF INVENTION: EPITOPE SEQUENCES
;  FILE REFERENCE: CTLIMM.027A
;  CURRENT APPLICATION NUMBER: US/10/117,937
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: US 60/282,211
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/337,017
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: US 60/363,210
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 602
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-117-937-74

  Query Match             100.0%;  Score 64;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.94;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 10
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US-10-295-027-386
; Sequence 386, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 386
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-386

Query Match 100.0%; Score 64; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARASGPGGGAPR 12
||||||||||||
Db 51 ARASGPGGGAPR 62

RESULT 11
US-10-296-734-832
; Sequence 832, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 832
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYNSO1a consensus polypeptide
US-10-296-734-832

Query Match 100.0%; Score 64; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARASGPGGGAPR 12
||||||||||||
Db 51 ARASGPGGGAPR 62

RESULT 12
US-10-188-832-139
; Sequence 139, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-139

Query Match 100.0%; Score 64; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARASGPGGGAPR 12
||||||||||||
Db 51 ARASGPGGGAPR 62

RESULT 13
US-10-777-053-11
; Sequence 11, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANNK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07

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;  PRIOR APPLICATION NUMBER: 60/336,968
;  PRIOR FILING DATE: 2001-11-07
;  NUMBER OF SEQ ID NOS: 979
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-777-053-11

  Query Match             100.0%;  Score 64;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.94;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 14
US-10-751-088-15
; Sequence 15, Application US/10751088
; Publication No. US20040158044A1
;   GENERAL INFORMATION:
;        APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
;                   Gure, Ali, Old, Lloyd, Ritter, Gerd
;        TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                            SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
;                            USES THEREOF
;        NUMBER OF SEQUENCES: 15
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FULBRIGHT & JAWORSKI LLP
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10158
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/751,088
;             FILING DATE: 02-Jan-2004
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/165,546D
;             FILING DATE: 02-Oct-1998
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: April 17, 1998
;             APPLICATION NUMBER: 08/937,263
;             FILING DATE: September 15, 1997
;             APPLICATION NUMBER: US 08/725,182
;             FILING DATE: October 3, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, Norman D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3000
;             TELEFAX: (212) 318-3400
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 180 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-10-751-088-15

  Query Match             100.0%;  Score 64;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.94;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


RESULT 15
US-10-657-022-74
; Sequence 74, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
;  APPLICANT: Simard, John J. L.
;  APPLICANT:  Diamond, David C.
;  APPLICANT:  Liu, Liping
;  APPLICANT:  Liu, Zheng
;  TITLE OF INVENTION: EPITOPE SEQUENCES
;  FILE REFERENCE: MANNK.032A
;  CURRENT APPLICATION NUMBER: US/10/657,022
;  CURRENT FILING DATE:  2003-09-04
;  PRIOR APPLICATION NUMBER: 60/409123
;  PRIOR FILING DATE: 2002-09-06
;  NUMBER OF SEQ ID NOS: 610
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-657-022-74

  Query Match             100.0%;  Score 64;  DB 4;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.94;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db         51 ARASGPGGGAPR 62


Search completed: March 13, 2006, 20:02:27
Job time : 72.5647 secs
```

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:54:06 ; Search time 8.18824 Seconds
(without alignments)
40.793 Million cell updates/sec

Title: US-09-529-206E-29
Perfect score: 64
Sequence: 1 ARASGPGGGAPR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	64	100.0	180	7	US-11-155-288-7	Sequence 7, Appli
2	64	100.0	240	7	US-11-021-441-28	Sequence 28, Appl
3	52	81.2	20	6	US-10-623-155-496	Sequence 496, App
4	47	73.4	306	7	US-11-096-568A-20556	Sequence 20556, A
5	46	71.9	134	7	US-11-096-568A-23806	Sequence 23806, A
6	45	70.3	678	7	US-11-072-512-3295	Sequence 3295, Ap
7	44	68.8	558	7	US-11-096-568A-26217	Sequence 26217, A
8	43	67.2	353	7	US-11-096-568A-22334	Sequence 22334, A
9	43	67.2	358	7	US-11-096-568A-22333	Sequence 22333, A
10	43	67.2	413	7	US-11-096-568A-27265	Sequence 27265, A
11	43	67.2	420	7	US-11-096-568A-22332	Sequence 22332, A
12	41	64.1	365	7	US-11-108-528-58	Sequence 58, Appl
13	41	64.1	537	7	US-11-179-958A-2	Sequence 2, Appli
14	41	64.1	555	7	US-11-072-512-3369	Sequence 3369, Ap
15	41	64.1	953	7	US-11-037-243-66	Sequence 66, Appl
16	40.5	63.3	280	7	US-11-143-980-34	Sequence 34, Appl
17	40	62.5	379	7	US-11-109-156-16	Sequence 16, Appl
18	40	62.5	974	6	US-10-531-036-35	Sequence 35, Appl
19	40	62.5	1832	7	US-11-087-099-7762	Sequence 7762, Ap
20	39	60.9	213	7	US-11-072-512-2722	Sequence 2722, Ap
21	39	60.9	233	7	US-11-240-769-58	Sequence 58, Appl
22	39	60.9	298	6	US-10-821-234-1240	Sequence 1240, Ap
23	39	60.9	430	6	US-10-992-577-8	Sequence 8, Appli
24	39	60.9	430	6	US-10-508-892-2	Sequence 2, Appli
25	39	60.9	430	7	US-11-223-294-54	Sequence 54, Appl
26	39	60.9	618	7	US-11-078-735-18	Sequence 18, Appl
27	39	60.9	618	7	US-11-050-346-63	Sequence 63, Appl
28	39	60.9	618	7	US-11-103-077-18	Sequence 18, Appl
29	39	60.9	662	7	US-11-072-175-184	Sequence 184, App
30	39	60.9	836	7	US-11-154-227-105	Sequence 105, App
31	39	60.9	904	7	US-11-154-227-97	Sequence 97, Appl
32	38.5	60.2	219	7	US-11-096-568A-1390	Sequence 1390, Ap
33	38	59.4	132	7	US-11-096-568A-14323	Sequence 14323, A
34	38	59.4	162	7	US-11-096-568A-641	Sequence 641, App
35	38	59.4	228	7	US-11-096-568A-16457	Sequence 16457, A
36	38	59.4	235	7	US-11-096-568A-1070	Sequence 1070, Ap
37	38	59.4	236	7	US-11-096-568A-22845	Sequence 22845, A
38	38	59.4	249	7	US-11-096-568A-23045	Sequence 23045, A
39	38	59.4	274	7	US-11-096-568A-22603	Sequence 22603, A
40	38	59.4	306	7	US-11-096-568A-12071	Sequence 12071, A
41	38	59.4	320	7	US-11-096-568A-988	Sequence 988, App
42	38	59.4	341	6	US-10-821-234-1628	Sequence 1628, Ap
43	38	59.4	438	6	US-10-650-326B-9	Sequence 9, Appli
44	38	59.4	459	7	US-11-096-568A-21887	Sequence 21887, A
45	38	59.4	830	6	US-10-921-793-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-11-155-288-7
; Sequence 7, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-7

Query Match 100.0%; Score 64; DB 7; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARASGPGGGAPR 12
||||||||||||
Db 51 ARASGPGGGAPR 62

RESULT 2
US-11-021-441-28
; Sequence 28, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06

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;  PRIOR APPLICATION NUMBER: US 60/615,287
;  PRIOR FILING DATE: 2004-10-01
;  PRIOR APPLICATION NUMBER: US 60/599,377
;  PRIOR FILING DATE: 2004-08-05
;  PRIOR APPLICATION NUMBER: PCT/US2004/23881
;  PRIOR FILING DATE: 2004-07-23
;  PRIOR APPLICATION NUMBER: US 10/883,599
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: US 60/556,744
;  PRIOR FILING DATE: 2004-03-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion protein
US-11-021-441-28

  Query Match            100.0%;  Score 64;  DB 7;  Length 240;
  Best Local Similarity  100.0%;  Pred. No. 0.04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||||||||||||
Db        111 ARASGPGGGAPR 122


RESULT 3
US-10-623-155-496
; Sequence 496, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Peckham, David W.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Fangef, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C20
;  CURRENT APPLICATION NUMBER: US/10/623,155
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 496
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-623-155-496

  Query Match            81.2%;  Score 52;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0.19;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGA 10
              ||||||||||
Db         11 ARASGPGGGA 20


RESULT 4
US-11-096-568A-20556
; Sequence 20556, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20556
;   LENGTH: 306
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(306)
;   OTHER INFORMATION: Ceres Seq. ID no. 12383286
US-11-096-568A-20556

  Query Match            73.4%;  Score 47;  DB 7;  Length 306;
  Best Local Similarity  81.8%;  Pred. No. 9.5;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAP 11
              ||| ||| |||
Db         91 ARADGPGTGAP 101


RESULT 5
US-11-096-568A-23806
; Sequence 23806, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23806
;   LENGTH: 134
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(134)
;   OTHER INFORMATION: Ceres Seq. ID no. 12415289
US-11-096-568A-23806

  Query Match            71.9%;  Score 46;  DB 7;  Length 134;
  Best Local Similarity  72.7%;  Pred. No. 6.4;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAP 11
              || :||| |||
Db         69 ARGAGPGAGAP 79


RESULT 6
US-11-072-512-3295
; Sequence 3295, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
;  APPLICANT: ISOGAI, TAKAO
;  APPLICANT:  SUGIYAMA, TOMOYASU
;  APPLICANT:  OTSUKI, TETSUJI
;  APPLICANT:  WAKAMATSU, AI
;  APPLICANT:  SATO, HIROYUKI
;  APPLICANT:  ISHII, SHIZUKO
;  APPLICANT:  YAMAMOTO, JUN-ICHI
;  APPLICANT:  ISONO, YUUKO
;  APPLICANT:  HIO, YURI
;  APPLICANT:  OTSUKA, KAORU
;  APPLICANT:  NAGAI, KEIICHI
;  APPLICANT:  IRIE, RYOTARO
;  APPLICANT:  TAMECHIKA, ICHIRO
;  APPLICANT:  SEKI, NAOHIKO
;  APPLICANT:  YOSHIKAWA, TSUTOMU
;  APPLICANT:  OTSUKA, MOTOYUKI
;  APPLICANT:  NAGAHARI, KENJI
;  APPLICANT:  MASUHO, YASUHIKO
;  TITLE OF INVENTION: Novel full length cDNA
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;  FILE REFERENCE: 084335-0191
;  CURRENT APPLICATION NUMBER: US/11/072,512
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: US 60/350,978
;  PRIOR FILING DATE: 2002-01-25
;  PRIOR APPLICATION NUMBER: JP 2001-379298
;  PRIOR FILING DATE: 2001-11-05
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3295
;   LENGTH: 678
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-072-512-3295

  Query Match             70.3%;  Score 45;  DB 7;  Length 678;
  Best Local Similarity   80.0%;  Pred. No. 35;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 RASGPGGGAP 11
              ||:||||| |
Db        592 RAAGPGGGWP 601


RESULT 7
US-11-096-568A-26217
; Sequence 26217, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26217
;   LENGTH: 558
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(558)
;   OTHER INFORMATION: Ceres Seq. ID no. 13498878
US-11-096-568A-26217

  Query Match             68.8%;  Score 44;  DB 7;  Length 558;
  Best Local Similarity   66.7%;  Pred. No. 41;
  Matches    8;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||  || || ||
Db        389 ARQEGPAGGEPR 400


RESULT 8
US-11-096-568A-22334
; Sequence 22334, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22334
;   LENGTH: 353
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(353)
;   OTHER INFORMATION: Ceres Seq. ID no. 12408544
US-11-096-568A-22334

  Query Match             67.2%;  Score 43;  DB 7;  Length 353;
  Best Local Similarity   66.7%;  Pred. No. 37;
  Matches    8;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||  ||||  ||
Db        109 ARGQGPGGEQPR 120


RESULT 9
US-11-096-568A-22333
; Sequence 22333, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22333
;   LENGTH: 358
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(358)
;   OTHER INFORMATION: Ceres Seq. ID no. 12408543
US-11-096-568A-22333

  Query Match             67.2%;  Score 43;  DB 7;  Length 358;
  Best Local Similarity   66.7%;  Pred. No. 38;
  Matches    8;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||  ||||  ||
Db        114 ARGQGPGGEQPR 125


RESULT 10
US-11-096-568A-27265
; Sequence 27265, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27265
;   LENGTH: 413
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(413)
;   OTHER INFORMATION: Ceres Seq. ID no. 15180691
US-11-096-568A-27265

  Query Match             67.2%;  Score 43;  DB 7;  Length 413;
  Best Local Similarity   72.7%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAP 11
              ||  |||| ||
Db         95 ARRRGPGGAAP 105
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```
RESULT 11
US-11-096-568A-22332
, Sequence 22332, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22332
;   LENGTH: 420
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(420)
;   OTHER INFORMATION: Ceres Seq. ID no. 12408542
US-11-096-568A-22332

  Query Match             67.2%;  Score 43;  DB 7;  Length 420;
  Best Local Similarity   66.7%;  Pred. No. 43;
  Matches    8;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ARASGPGGGAPR 12
              ||  ||||  ||
Db        176 ARGQGPGGEQPR 187


RESULT 12
US-11-108-528-58
; Sequence 58, Application US/11108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
;  APPLICANT: Larsen, Glenn
;  APPLICANT:  Marvin, Martha
;  APPLICANT:  Li, Dean Y.
;  APPLICANT:  Wang, Elizabeth
;  APPLICANT:  Chen, C. M. Amy
;  APPLICANT:  Shamah, Steven M.
;  TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
;  TITLE OF INVENTION:  PROLIFERATION
;  FILE REFERENCE: HYDR-P01-041
;  CURRENT APPLICATION NUMBER: US/11/108,528
;  CURRENT FILING DATE:  2005-04-18
;  PRIOR APPLICATION NUMBER: US 60/563,137
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 60/598,368
;  PRIOR FILING DATE: 2004-08-02
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 58
;   LENGTH: 365
;   TYPE: PRT
;   ORGANISM: Mouse
US-11-108-528-58

  Query Match             64.1%;  Score 41;  DB 7;  Length 365;
  Best Local Similarity   80.0%;  Pred. No. 71;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 RASGPGGGAP 11
              |||| ||| |
Db        273 RASGSGGGDP 282


RESULT 13
US-11-179-958A-2
; Sequence 2, Application US/11179958A
; Publication No. US20060030537A1
; GENERAL INFORMATION:
;  APPLICANT: Chalfant, Charles E.
;  APPLICANT:  Hannun, Yusef A.
;  APPLICANT:  Pettus, Benjamin J.
;  APPLICANT:  Bielawska, Alicja
;  TITLE OF INVENTION: Ceramide Kinase and Uses Thereof
;  FILE REFERENCE: 9175-028-999 (MUSC Ref P0401)
;  CURRENT APPLICATION NUMBER: US/11/179,958A
;  CURRENT FILING DATE:  2005-07-11
;  PRIOR APPLICATION NUMBER: 60/586,909
;  PRIOR FILING DATE: 2004-07-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 537
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Human ceramide kinase
US-11-179-958A-2

  Query Match             64.1%;  Score 41;  DB 7;  Length 537;
  Best Local Similarity   70.0%;  Pred. No. 99;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 RASGPGGGAP 11
              |: ||| |||
Db         36 RSPGPGAGAP 45


RESULT 14
US-11-072-512-3369
; Sequence 3369, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
;  APPLICANT: ISOGAI, TAKAO
;  APPLICANT:  SUGIYAMA, TOMOYASU
;  APPLICANT:  OTSUKI, TETSUJI
;  APPLICANT:  WAKAMATSU, AI
;  APPLICANT:  SATO, HIROYUKI
;  APPLICANT:  ISHII, SHIZUKO
;  APPLICANT:  YAMAMOTO, JUN-ICHI
;  APPLICANT:  ISONO, YUUKO
;  APPLICANT:  HIO, YURI
;  APPLICANT:  OTSUKA, KAORU
;  APPLICANT:  NAGAI, KEIICHI
;  APPLICANT:  IRIE, RYOTARO
;  APPLICANT:  TAMECHIKA, ICHIRO
;  APPLICANT:  SEKI, NAOHIKO
;  APPLICANT:  YOSHIKAWA, TSUTOMU
;  APPLICANT:  OTSUKA, MOTOYUKI
;  APPLICANT:  NAGAHARI, KENJI
;  APPLICANT:  MASUHO, YASUHIKO
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: 084335-0191
;  CURRENT APPLICATION NUMBER: US/11/072,512
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: US 60/350,978
;  PRIOR FILING DATE: 2002-01-25
;  PRIOR APPLICATION NUMBER: JP 2001-379298
;  PRIOR FILING DATE: 2001-11-05
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3369
;   LENGTH: 555
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-072-512-3369

  Query Match             64.1%;  Score 41;  DB 7;  Length 555;
  Best Local Similarity   77.8%;  Pred. No. 1e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          3 ASGPGGGAP 11
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Db        473 ASGPGSGSP 481


RESULT 15
US-11-037-243-66
; Sequence 66, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY
;  APPLICANT:  WHYTE, DAVID
;  APPLICANT:  CAENEPEEL, SEAN
;  APPLICANT:  CHARYDCZAK, GLEN
;  APPLICANT:  MANNING, GERARD
;  APPLICANT:  SUDARSANAM, SUCHA
;  TITLE OF INVENTION: NOVEL PROTEASES
;  FILE REFERENCE: 038602/1214
;  CURRENT APPLICATION NUMBER: US/11/037,243
;  CURRENT FILING DATE:  2005-05-26
;  PRIOR APPLICATION NUMBER: US/09/888,615
;  PRIOR FILING DATE: 2001-06-26
;  PRIOR APPLICATION NUMBER: 60/214,047
;  PRIOR FILING DATE: 2000-06-26
;  NUMBER OF SEQ ID NOS: 150
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
;   LENGTH: 953
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-037-243-66

  Query Match             64.1%;  Score 41;  DB 7;  Length 953;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GPGGGAPR 12
              ||||| ||
Db        214 GPGGGHPR 221


Search completed: March 13, 2006, 20:03:31
Job time : 8.18824 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 18:52:59 ; Search time 82.8235 Seconds
(without alignments)
58.355 Million cell updates/sec

Title: US-09-529-206E-30
Perfect score: 60
Sequence: 1 RASGPGGGAPR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	60	100.0	11	2	AAY06066	Aay06066 Human can
2	60	100.0	12	2	AAY06065	Aay06065 Human can
3	60	100.0	13	2	AAY06064	Aay06064 Human can
4	60	100.0	14	2	AAY05986	Aay05986 Human can
5	60	100.0	15	2	AAY05978	Aay05978 Human can
6	60	100.0	20	2	AAY05979	Aay05979 Human can
7	60	100.0	30	5	AAU85105	Aau85105 Human NYN
8	60	100.0	179	8	ADK68648	Adk68648 Epitope l
9	60	100.0	180	2	AAW62584	Aaw62584 Cancer as
10	60	100.0	180	2	AAW69665	Aaw69665 Human NY-
11	60	100.0	180	2	AAY05965	Aay05965 Human can
12	60	100.0	180	3	AAY52430	Aay52430 Human tum
13	60	100.0	180	3	AAY70862	Aay70862 Human tum
14	60	100.0	180	3	AAB03154	Aab03154 Human oes
15	60	100.0	180	4	AAB69946	Aab69946 Human NY-
16	60	100.0	180	4	AAG67164	Aag67164 Amino aci
17	60	100.0	180	4	AAU01535	Aau01535 Human NY-
18	60	100.0	180	4	AAE07714	Aae07714 Human NY
19	60	100.0	180	5	AAU84818	Aau84818 Human NYN
20	60	100.0	180	5	AAU11543	Aau11543 Human tum
21	60	100.0	180	6	ABR58672	Abr58672 Human can
22	60	100.0	180	6	ABR48210	Abr48210 Human bla
23	60	100.0	180	6	ABU56508	Abu56508 Lung canc
24	60	100.0	180	6	ABU56694	Abu56694 Lung canc
25	60	100.0	180	6	ABP74198	Abp74198 Human NY-
26	60	100.0	180	6	ABU64816	Abu64816 Human NY-
27	60	100.0	180	6	ABR83438	Abr83438 Human NY-
28	60	100.0	180	7	ADC09576	Adc09576 NY-ESO-1
29	60	100.0	180	7	ADD35564	Add35564 Human NY-
30	60	100.0	180	7	ADD35568	Add35568 Human NY-
31	60	100.0	180	7	ADD25510	Add25510 Binding d
32	60	100.0	180	7	ADN39068	Adn39068 Cancer/an
33	60	100.0	180	8	ADJ54139	Adj54139 Human NY-
34	60	100.0	180	8	ADM72815	Adm72815 Human NY-
35	60	100.0	180	8	ADM73418	Adm73418 CAG-3 pro
36	60	100.0	180	8	ADM73417	Adm73417 Human NY-
37	60	100.0	180	8	ADQ18451	Adq18451 Human sof
38	60	100.0	180	8	ADQ10446	Adq10446 Autoimmun
39	60	100.0	180	8	ADS80926	Ads80926 Tumour as
40	60	100.0	180	9	ADW44353	Adw44353 Human aut
41	60	100.0	180	9	ADY85096	Ady85096 Tumor ant
42	60	100.0	180	9	ADZ28913	Adz28913 NY-ESO-1
43	60	100.0	180	9	ADZ42374	Adz42374 Immunogen
44	60	100.0	180	9	AEA35651	Aea35651 Human NY-
45	60	100.0	240	9	ADW99402	Adw99402 NY-ESO-1/

ALIGNMENTS

RESULT 1
AAY06066
ID AAY06066 standard; peptide; 11 AA.
XX
AC AAY06066;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 peptide.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Example 11; Page 50; 88pp; English.
XX
CC This peptide corresponds to amino acid residues 52-62 of human NY ESO-
CC 1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is
CC capable of eliciting an antigen specific immune response by T cells.
CC Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3
CC and their variants, are useful as cancer vaccines. A claimed method of
CC preventing or inhibiting cancer involves administering a cancer peptide,
CC with or without an HLA molecule. The cancer peptides form part of, or are
CC derived from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,

```
CC   cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC   as breast, prostate, ovarian, pancreatic and thyroid cancers
XX
SQ   Sequence 11 AA;

  Query Match             100.0%;  Score 60;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||
Db          1 RASGPGGGAPR 11


RESULT 2
AAY06065
ID   AAY06065 standard; peptide; 12 AA.
XX
AC   AAY06065;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 peptide.
XX
KW   NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW   leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW   metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW   uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW   cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW   liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW   vaccine; cytotoxic T lymphocyte; CTL.
XX
OS   Homo sapiens.
XX
PN   WO9918206-A2.
XX
PD   15-APR-1999.
XX
PF   21-SEP-1998;   98WO-US019609.
XX
PR   08-OCT-1997;   97US-0061428P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang RF,  Rosenberg SA;
XX
DR   WPI; 1999-277270/23.
XX
PT   Cancer antigen NY ESO1/CAG-3.
XX
PS   Example 11; Page 50; 88pp; English.
XX
CC   This peptide corresponds to amino acid residues 51-62 of human NY ESO-
CC   1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is
CC   capable of eliciting an antigen specific immune response by T cells.
CC   Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3
CC   and their variants, are useful as cancer vaccines. A claimed method of
CC   preventing or inhibiting cancer involves administering a cancer peptide,
CC   with or without an HLA molecule. The cancer peptides form part of, or are
CC   derived from, cancers such as primary or metastatic melanoma, thymoma,
CC   lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC   cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC   as breast, prostate, ovarian, pancreatic and thyroid cancers
XX
SQ   Sequence 12 AA;

  Query Match             100.0%;  Score 60;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||
Db          2 RASGPGGGAPR 12


RESULT 3
AAY06064
ID   AAY06064 standard; peptide; 13 AA.
XX
AC   AAY06064;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 peptide.
XX
KW   NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW   leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW   metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW   uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW   cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW   liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW   vaccine; cytotoxic T lymphocyte; CTL.
XX
OS   Homo sapiens.
XX
PN   WO9918206-A2.
XX
PD   15-APR-1999.
XX
PF   21-SEP-1998;   98WO-US019609.
XX
PR   08-OCT-1997;   97US-0061428P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang RF,  Rosenberg SA;
XX
DR   WPI; 1999-277270/23.
XX
PT   Cancer antigen NY ESO1/CAG-3.
XX
PS   Example 11; Page 50; 88pp; English.
XX
CC   This peptide corresponds to amino acid residues 50-62 of human NY ESO-
CC   1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is
CC   capable of eliciting an antigen specific immune response by T cells.
CC   Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3
CC   and their variants, are useful as cancer vaccines. A claimed method of
CC   preventing or inhibiting cancer involves administering a cancer peptide,
CC   with or without an HLA molecule. The cancer peptides form part of, or are
CC   derived from, cancers such as primary or metastatic melanoma, thymoma,
CC   lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC   cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC   as breast, prostate, ovarian, pancreatic and thyroid cancers
XX
SQ   Sequence 13 AA;

  Query Match             100.0%;  Score 60;  DB 2;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||
Db          3 RASGPGGGAPR 13


RESULT 4
AAY05986
ID   AAY05986 standard; peptide; 14 AA.
XX
AC   AAY05986;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
```

KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Claim 25; Page 50; 88pp; English.
XX
CC The present sequence represents a cancer peptide that corresponds to
CC amino acid residues 49-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
CC AAY05965), a new and potent tumour antigen capable of eliciting an
CC antigen specific immune response by T cells. Cancer peptides derived from
CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
CC variants (see AAY05967-87), are useful as cancer vaccines that protect
CC against cancer. The invention provides: vectors and host cells (also
CC useful as vaccines); a method of diagnosis of cancer or precancer; a
CC transgenic animal; antisense oligonucleotides that inhibit expression of
CC the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
CC cancer peptide, useful in diagnostic and detection assays; and methods
CC for preventing or inhibiting cancer by administering a cancer peptide,
CC with or without an HLA molecule. The cancer peptides form part of, or are
CC derived from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
CC treated by inducing cancer-specific T cells in vitro for subsequent
CC return to a patient
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 60; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASGPGGGAPR 11
||||||||||||
Db 4 RASGPGGGAPR 14

RESULT 5
AAY05978
ID AAY05978 standard; peptide; 15 AA.
XX
AC AAY05978;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Claim 15; Page 64; 88pp; English.
XX
CC The present sequence represents a cancer peptide that corresponds to
CC amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
CC AAY05965), a new and potent tumour antigen capable of eliciting an
CC antigen specific immune response by T cells. Cancer peptides derived from
CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
CC variants (see AAY05967-87), are useful as cancer vaccines that protect
CC against cancer. The invention provides: vectors and host cells (also
CC useful as vaccines); a method of diagnosis of cancer or precancer; a
CC transgenic animal; antisense oligonucleotides that inhibit expression of
CC the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
CC cancer peptide, useful in diagnostic and detection assays; and methods
CC for preventing or inhibiting cancer by administering a cancer peptide,
CC with or without an HLA molecule. The cancer peptides form part of, or are
CC derived from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
CC treated by inducing cancer-specific T cells in vitro for subsequent
CC return to a patient
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 60; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASGPGGGAPR 11
||||||||||||
Db 5 RASGPGGGAPR 15

RESULT 6
AAY05979
ID AAY05979 standard; peptide; 20 AA.
XX
AC AAY05979;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine.
XX

OS Homo sapiens.
OS Synthetic.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Claim 16; Page 64; 88pp; English.
XX
CC The present sequence represents a cancer peptide that is based on amino
CC acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965),
CC a new and potent tumour antigen capable of eliciting an antigen specific
CC immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-
CC 3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-
CC 87), are useful as cancer vaccines that protect against cancer. The
CC invention provides: vectors and host cells (also useful as vaccines); a
CC method of diagnosis of cancer or precancer; a transgenic animal;
CC antisense oligonucleotides that inhibit expression of the cancer peptide
CC or tumour antigen; antibodies reacting with a CAG-3 cancer peptide,
CC useful in diagnostic and detection assays; and methods for preventing or
CC inhibiting cancer by administering a cancer peptide, with or without an
CC HLA molecule. The cancer peptides form part of, or are derived from,
CC cancers such as primary or metastatic melanoma, thymoma, lymphoma,
CC sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
CC cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
CC prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by
CC inducing cancer-specific T cells in vitro for subsequent return to a
CC patient
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 60; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASGPGGGAPR 11
||||||||||
Db 10 RASGPGGGAPR 20

RESULT 7
AAU85105
ID AAU85105 standard; peptide; 30 AA.
XX
AC AAU85105;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human NYNSO1a segment 4.
XX
KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW viral infection; human immunodeficieny virus; melanoma;
KW bacterial infection; Salmonella; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
XX
OS Homo sapiens.
XX
PN WO200190197-A1.
XX
PD 29-NOV-2001.
XX
PF 25-MAY-2001; 2001WO-AU000622.
XX
PR 26-MAY-2000; 2000AU-00007761.
XX
PA (AUSU) UNIV AUSTRALIAN NAT.
XX
PI Thomson SA, Ramshaw IA;
XX
DR WPI; 2002-147575/19.
DR N-PSDB; ABK36925.
XX
PT New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
PS Example 3; Fig 27; 364pp; English.
XX
CC The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention
XX
SQ Sequence 30 AA;

Query Match 100.0%; Score 60; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASGPGGGAPR 11
||||||||||
Db 9 RASGPGGGAPR 19

RESULT 8
ADK68648
ID ADK68648 standard; protein; 179 AA.
XX
AC ADK68648;
XX
DT 06-MAY-2004 (first entry)
XX
DE Epitope liberation-related NY-ESO-1 protein SeqID11.
XX
KW epitope liberation; substrate; proteasome; cytostatic; antibacterial;
KW protozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope;
KW cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;
KW virus; bacterium; protozoan; fungus; housekeeping proteasome system;
KW human.
XX
OS Homo sapiens.
XX
PN US2003228634-A1.
XX

```
PD   11-DEC-2003.
XX
PF   07-NOV-2002; 2002US-00292413.
XX
PR   07-NOV-2001; 2001US-0336968P.
XX
PA   (SIMA/) SIMARD J J L.
PA   (DIAM/) DIAMOND D C.
PA   (QIUZ/) QIU Z.
PA   (LEIX/) LEI X.
XX
PI   Simard JJL,  Diamond DC,  Qiu Z,  Lei X;
XX
DR   WPI; 2004-167209/16.
DR   N-PSDB; ADK68674.
XX
PT   Identifying polypeptide suitable for epitope e.g., housekeeping epitope,
PT   liberation by contacting substrate polypeptide comprising epitope of
PT   interest, with proteasome, and assaying for liberation of epitope.
XX
PS   Example 2; SEQ ID NO 11; 67pp; English.
XX
CC   This invention relates to a novel method of identifying a polypeptide
CC   suitable for epitope liberation, including the steps of identifying an
CC   epitope of interest; providing substrate polypeptide sequence including
CC   the epitope, wherein the substrate permits processing by a proteasome;
CC   contacting the substrate with a composition including the proteasome,
CC   under conditions that support processing of the substrate by proteasome;
CC   and assaying for liberation of epitope. The invention may be useful for
CC   the development of compounds with a cytostatic, antibacterial,
CC   protozoacide or fungicide activity acting as T-cell activators. In
CC   addition, the invention may allow development of a vaccine. The invention
CC   is useful for identifying a polypeptide suitable for epitope liberation,
CC   where the epitope is a housekeeping epitope. The compositions comprising
CC   the identified housekeeping epitopes are useful in vitro in vaccine
CC   development or in the generation or expansion of cytotoxic T lymphocyte
CC   (CTL) to be used in adoptive immunotherapy. The invention is also useful
CC   for activating T-cells against neoplastic cells, and cells infected with
CC   virus, bacterium, protozoan or fungus. CTL epitopes are identified based
CC   on the knowledge that such epitopes are, in fact, produced by the
CC   housekeeping proteasome system. Once identified, these epitopes, embodied
CC   as peptides, can be used to successfully immunise or induce therapeutic
CC   CTL responses against housekeeping proteasome expressing target cells in
CC   the host. The present sequence is that of a protein which is related to
CC   the method of the invention.
XX
SQ   Sequence 179 AA;

  Query Match           100.0%;  Score 60;  DB 8;  Length 179;
  Best Local Similarity  100.0%;  Pred. No. 1.5;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||| 
Db         51 RASGPGGGAPR 61


RESULT 9
AAW62584
ID   AAW62584 standard; protein; 180 AA.
XX
AC   AAW62584;
XX
DT   17-SEP-1998  (first entry)
XX
DE   Cancer associated antigen NY-ESO-1.
XX
KW   Cancer associated antigen; NY-ESO-1; regression; progression; onset;
KW   cancer; treatment; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 7
FT                   /note= "potential myristorylation site"
FT   Misc-difference 9
FT                   /note= "potential myristorylation site"
FT   Misc-difference 11
FT                   /note= "potential phosphorylation site"
FT   Misc-difference 98
FT                   /note= "potential phosphorylation site"
FT   Misc-difference 134
FT                   /note= "potential phosphorylation site"
FT   Misc-difference 138
FT                   /note= "potential phosphorylation site"
XX
PN   WO9814464-A1.
XX
PD   09-APR-1998.
XX
PF   15-SEP-1997;   97WO-US016335.
XX
PR   03-OCT-1996;   96US-00725182.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Chen Y,  Scanlan M,  Gure A,  Old LJ,  Jager E,  Knuth A;
PI   Drijfhout JW;
XX
DR   WPI; 1998-286417/25.
DR   N-PSDB; AAV38566.
XX
PT   New isolated cancer associated antigen - is used to develop products for
PT   the diagnosis and treatment of cancers and for monitoring cancer therapy.
XX
PS   Claim 8; Fig 3; 49pp; English.
XX
CC   The present sequence represents a cancer associated antigen. The clone
CC   from which the DNA sequence is obtained is designated NY-ESO-1. The
CC   specification described a method for determining regression, progression
CC   of onset of a cancerous condition, comprising monitoring a sample from a
CC   patient with the cancerous condition for a parameter selected from NY-ESO
CC   -1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells
CC   specific for the peptide and an MHC molecule with which it non-covalently
CC   complexes. Methods for the treatment of a cancerous condition are also
CC   described. The NY-ESO-1 protein and peptides derived from it can be used
CC   for diagnosis and treatment of cancers and to monitor the efficacy of a
CC   therapeutic regime
XX
SQ   Sequence 180 AA;

  Query Match           100.0%;  Score 60;  DB 2;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 1.5;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||| 
Db         52 RASGPGGGAPR 62


RESULT 10
AAW69665
ID   AAW69665 standard; protein; 180 AA.
XX
AC   AAW69665;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
XX
KW   Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
XX
OS   Homo sapiens.
XX
PN   WO9832855-A1.
XX
```

```
PD   30-JUL-1998.
XX
PF   27-JAN-1998;   98WO-US001445.
XX
PR   27-JAN-1997;   97US-00791495.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Lethe B,  Lucas S,  De Smet C,  Godelaine D,  Boon-Falleur T;
XX
DR   WPI; 1998-427951/36.
DR   N-PSDB; AAV50348.
XX
PT   New isolated LAGE-1 tumour associated nucleic acids - used to develop
PT   products for the diagnosis and treatment of LAGE-1 associated disorders,
PT   particularly tumours.
XX
PS   Example 2; Page 57-58; 73pp; English.
XX
CC   The present sequence represents human NY-ESO-1, formerly known as LL-1.2
CC   clone, which is used in an example from the present invention which
CC   describes LAGE-1 tumour associated protein (TAP). The present invention
CC   also describes: (1) a method for treating a subject with a disorder
CC   characterised by expression of a LAGE-1 nucleic acid molecule or an
CC   expression product, comprising administering to the subject autologous
CC   cytolytic T cells to ameliorate the disorder, where the cytolytic T cells
CC   are specific for complexes of an HLA molecule and a LAGE-1 TAP or an
CC   immunogenic fragment; (2) a method for treating a subject with a disorder
CC   characterised by expression of a LAGE-1 nucleic acid molecule or an
CC   expression product, comprising administering a LAGE-1 TAP or an
CC   immunogenic fragment to ameliorate the disorder; and (3) a method for
CC   selectively enriching a population of T cells with cytolytic T cells
CC   specific for a LAGE-1 TAP comprising contacting an isolated population of
CC   T cells with an agent presenting a complex of a LAGE TAP or an
CC   immunogenic fragment and a HLA presenting molecule to selectively enrich
CC   the isolated population of T cells with the cytolytic T cells. The
CC   methods and products from the present invention can be used for the
CC   diagnosis and treatment of LAGE-1 associated disorders, particularly
CC   tumours
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 60;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||
Db         52 RASGPGGGAPR 62


RESULT 11
AAY05965
ID   AAY05965 standard; protein; 180 AA.
XX
AC   AAY05965;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.
XX
KW   NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia;
KW   non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis;
KW   melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer;
KW   breast cancer; prostate cancer; ovarian cancer; cervical cancer;
KW   bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma;
KW   tumour; diagnosis; immunotherapy; therapy; vaccine; ORF1.
XX
OS   Homo sapiens.
XX
PN   WO9918206-A2.
XX
PD   15-APR-1999.
XX
PF   21-SEP-1998;   98WO-US019609.
XX
PR   08-OCT-1997;   97US-0061428P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Wang RF,  Rosenberg SA;
XX
DR   WPI; 1999-277270/23.
DR   N-PSDB; AAX58599.
XX
PT   Cancer antigen NY ESO1/CAG-3.
XX
PS   Claim 4; Fig 3A; 88pp; English.
XX
CC   The present sequence represents the ORF1 protein encoded by open reading
CC   frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and
CC   potent tumour antigen capable of eliciting an antigen specific immune
CC   response by T cells. Cancer peptides comprising ORF1, ORF2 (see
CC   AAY05966), portions of these peptides and their variants (see AAY05965-
CC   87), are useful as cancer vaccines that protect the recipient from
CC   development of cancer. The invention provides: vectors and host cells
CC   (also useful as vaccines); a method of diagnosis of cancer or precancer;
CC   a transgenic animal; antisense oligonucleotides that inhibit expression
CC   of the cancer peptide or tumour antigen; antibodies reacting with the CAG
CC   -3 cancer peptide, useful in diagnostic and detection assays; and methods
CC   for preventing or inhibiting cancer by administering a cancer peptide,
CC   with or without an HLA molecule. The cancer peptides form part of, or are
CC   derived from, cancers such as primary or metastatic melanoma, thymoma,
CC   lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC   cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC   as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
CC   treated by inducing cancer-specific T cells in vitro for subsequent
CC   return to a patient
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 60;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||
Db         52 RASGPGGGAPR 62


RESULT 12
AAY52430
ID   AAY52430 standard; protein; 180 AA.
XX
AC   AAY52430;
XX
DT   21-OCT-2004  (revised)
DT   15-FEB-2000  (first entry)
XX
DE   Human tumour antigen NY-ESO-1.
XX
KW   Cancer; tumour; antigen; MHC; major histocompatility complex; T-cell;
KW   cytotoxic; helper; stimulation; proliferation; treatment; diagnosis;
KW   prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;
KW   hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Peptide         44. .53
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         60. .69
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         60. .68
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
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```
FT   Peptide         63. .72
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         79. .88
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         79. .87
FT                   /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
FT                   and HLA-B35"
FT   Peptide         82. .91
FT                   /note= "Peptide presented by MHC Class I HLA-A1"
FT   Peptide         82. .90
FT                   /note= "Peptide presented by MHC Class I HLA-A1"
FT   Peptide         83. .91
FT                   /note= "Peptide presented by MHC Class I HLA-B44"
FT   Peptide         84. .92
FT                   /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
FT                   and HLA-B35"
FT   Peptide         87. .96
FT                   /note= "Peptide presented by MHC Class I HLA-A1"
FT   Peptide         88. .96
FT                   /note= "Peptide presented by MHC Class I HLA-B44"
FT   Peptide         96. .104
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         100. .108
FT                   /note= "Peptide presented by MHC Class I HLA-B44"
FT   Peptide         102. .110
FT                   /note= "Peptide presented by MHC Class I HLA-B44"
FT   Peptide         107. .116
FT                   /note= "Peptide presented by MHC Class I HLA-A24"
FT   Peptide         110. .118
FT                   /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide         113. .122
FT                   /note= "Peptide presented by MHC Class I HLA-B7 and HLA-
FT                   B52"
FT   Peptide         113. .121
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         115. .124
FT                   /note= "Peptide presented by MHC Class I HLA-A3"
FT   Peptide         118. .126
FT                   /note= "Peptide presented by MHC Class I HLA-B35"
FT   Peptide         124. .133
FT                   /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide         125. .133
FT                   /note= "Peptide presented by MHC Class I HLA-A24"
FT   Peptide         138. .147
FT                   /note= "Peptide presented by MHC Class I HLA-B8"
FT   Peptide         139. .147
FT                   /note= "Peptide presented by MHC Class I HLA-B7"
FT   Peptide         145. .153
FT                   /note= "Peptide presented by MHC Class I HLA-A24 and HLA-
FT                   B52"
FT   Peptide         153. .162
FT                   /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide         154. .163
FT                   /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide         154. .162
FT                   /note= "Peptide presented by MHC Class I HLA-B52"
FT   Peptide         156. .167
FT                   /note= "Peptide (AAY52434) presented by MHC Class I HLA-
FT                   A2"
FT   Peptide         158. .166
FT                   /note= "Peptide presented by MHC Class I HLA-A3"
FT   Peptide         159. .167
FT                   /note= "Peptide presented by MHC Class I HLA-A3"
FT   Peptide         162. .170
FT                   /note= "Peptide presented by MHC Class I HLA-B52"
XX
PN   WO9953938-A1.
XX
PD   28-OCT-1999.
XX
PF   24-MAR-1999;    99WO-US006875.
XX
PR   17-APR-1998;    98US-00062422.
PR   02-OCT-1998;    98US-00165546.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI   Gure A, Ritter G;
XX
DR   WPI; 2000-038483/03.
DR   N-PSDB; AAZ38380.
XX
PT   Novel peptides which bind to MHC class I and MHC class II molecules,
PT   useful for therapeutic and diagnostic purposes.
XX
PS   Claim 30; Fig 3; 49pp; English.
XX
CC   This sequence represents a human tumour antigen, NY-ESO-1, the cDNA
CC   encoding which was isolated from an oesophagus squamous cell cancer cDNA
CC   library. Tissue localisation studies revealed it to be expressed at high
CC   levels in normal ovary and testis but not in normal colon, kidney, liver,
CC   brain, oesophagus and skin. It was expressed in certain tumours and
CC   tumour cell lines with some degree of frequency - these included melanoma
CC   specimens and cell lines, and breast and bladder cancer specimens, with
CC   expression in other tumour types being sporadic. Peptides derived from NY
CC   -ESO-1 are bound by both MHC (major histocompatibility complex) Class I
CC   and Class II molecules for presentation to T-cells. Peptides AAY52431-
CC   Y52434 bind to Class I HLA-A2 molecules, thereby stimulating
CC   proliferation of cytotoxic T-cells, while peptides AAY52435-Y52440 bind
CC   to Class II HLA-DR53 molecules, stimulating helper T-cell proliferation.
CC   The peptides derived from NY-ESO-1 may be used in methods and
CC   compositions used for the treatment, diagnosis and prevention of cancers
CC   (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma,
CC   ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to
CC   stimulate the proliferation of T cells
CC
CC   Revised record issued on 21-OCT-2004 : Correction to feature table key
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 60;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||| 
Db         52 RASGPGGGAPR 62


RESULT 13
AAY70862
ID   AAY70862 standard; protein; 180 AA.
XX
AC   AAY70862;
XX
DT   31-JUL-2000  (first entry)
XX
DE   Human tumour antigen, NY-ESO-1 protein.
XX
KW   NY-ESO-1; CAMEL; CTL-recognised Antigen on MELanoma; human; cancer; CTL;
KW   cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer;
KW   melanoma; immunotherapy; immune response.
XX
OS   Homo sapiens.
XX
PN   WO200023584-A1.
XX
PD   27-APR-2000.
XX
PF   15-OCT-1999;    99WO-EP007832.
XX
PR   16-OCT-1998;    98EP-00119583.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA   (UYHO-) UNIV HOSPITAL LEIDEN.
```

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XX
PI   Schrier PI,  Aarnoudse CA,  Heider K,  Klade C;
XX
DR   WPI; 2000-339685/29.
DR   N-PSDB; AAD00152.
XX
PT   Tumor-associated antigen useful for cancer immunotherapy is encoded by
PT   the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
XX
PS   Example 3; Page 62-63; 73pp; English.
XX
CC   The present sequence is the human NY-ESO-1 protein, a tumour antigen,
CC   identified by screening an esophagus carcinoma cDNA library. This protein
CC   is derived from open reading frame (ORF)-1 that contain epitopes of
CC   tumour specific T-cells. NY-ESO-1 is expressed in different tumour types,
CC   but not in healthy tissues except in testis. It also shows homology with
CC   the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELanoma)
CC   protein, a tumour-asociated antigen. The tumour-associated antigen
CC   displayed on melanoma cells is recognised by cytotoxic T lymphocytes.
CC   This sequence has anticancer activity. CAMEL tumour antigen and
CC   immunogenic peptides derived from it are useful for cancer immunotherapy.
CC   They have the potential to induce an immune response, by eliciting a CTL
CC   response. The DNA molecule is used for the construction of recombinant or
CC   fusion proteins
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 60;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||| 
Db         52 RASGPGGGAPR 62


RESULT 14
AAB03154
ID   AAB03154 standard; protein; 180 AA.
XX
AC   AAB03154;
XX
DT   23-OCT-2000  (first entry)
XX
DE   Human oesophageal cancer-associated antigen NY-ESO-1.
XX
KW   Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen;
KW   oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain;
KW   antibody; diagnostic marker; drug delivery target.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   7
FT                   /note= "Potential N-myristoylation site"
FT   Modified-site   9
FT                   /note= "Potential N-myristoylation site"
FT   Modified-site   11
FT                   /note= "Potential O-phosphorylation site"
FT   Modified-site   98
FT                   /note= "Potential O-phosphorylation site"
FT   Modified-site   134
FT                   /note= "Potential O-phosphorylation site"
FT   Modified-site   138
FT                   /note= "Potential O-phosphorylation site"
FT   Domain          152. .172
FT                   /note= "Potential transmembrane domain"
XX
PN   US6069233-A.
XX
PD   30-MAY-2000.
XX
PF   26-JAN-1998;   98US-00013150.
XX
PR   03-OCT-1996;   96US-00725381.
XX
PA   (SLOK ) SLOAN KETTERING INST CANCER RES.
PA   (CORR ) CORNELL RES FOUND INC.
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Scanlan M,  Gure AO,  Chen Y,  Tureci O,  Sahin U,  Pfreundschuh M;
PI   Old LJ;
XX
DR   WPI; 2000-410880/35.
DR   N-PSDB; AAA61483.
XX
PT   New isolated esophageal cancer-associated antigen useful as markers for
PT   producing antibodies and as targets for identifying abnormal conditions,
PT   e.g. infections and cancer.
XX
PS   Example 5; Fig 3; 9pp; English.
XX
CC   This sequence represents a human oesophageal cancer-associated antigen,
CC   NY-ESO-1. The cDNA encoding this sequence was isolated from a cDNA
CC   library prepared from a specimen of well-to-moderately differentiated
CC   squamous cell cancer of the oesophagus. Expression analysis demonstrated
CC   that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma
CC   cell lines and in normal ovary and testis tissue, but not in normal
CC   colon, kidney, liver or brain tissue. Analysis of the amino acid sequence
CC   of the protein indicates that the protein has a transmembrane domain,
CC   several N-myristoylation sites and O-phosphorylation sites and that it
CC   contains antigenic sequences in the N-terminal half of the protein. The
CC   antigen is useful as an immunogen when combined with an adjuvant, in both
CC   precursor and post- translationally modified forms, and may be used to
CC   generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic
CC   marker for oesophageal cancer, and can be utilised as a marker for the
CC   targetted delivery of therapeutic agents to oesophageal cancer cells. It
CC   can also be used to generate diagnostic or therapeutic agents
XX
SQ   Sequence 180 AA;

  Query Match             100.0%;  Score 60;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||| 
Db         52 RASGPGGGAPR 62


RESULT 15
AAB69946
ID   AAB69946 standard; protein; 180 AA.
XX
AC   AAB69946;
XX
DT   27-APR-2001  (first entry)
XX
DE   Human NY-ESO-1 protein.
XX
KW   Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW   HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW   non-small cell lung carcinoma; tumour status determination.
XX
OS   Homo sapiens.
XX
PN   WO200107917-A1.
XX
PD   01-FEB-2001.
XX
PF   14-JUL-2000; 2000WO-US019220.
XX
PR   23-JUL-1999;   99US-00359503.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (SLOK ) SLOAN KETTERING INST CANCER RES.
```

PA (CORR) CORNELL RES FOUND INC.
XX
PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX
DR WPI; 2001-182822/18.
DR N-PSDB; AAF58634.
XX
PT Method useful for determining the status (e.g. progression, regression or
PT stability of the disease) of a cancerous condition, involves determining
PT the levels of NY-ESO-1 specific antibodies in a sample taken from a
PT patient.
XX
PS Example 5; Fig 3; 50pp; English.
XX
CC The present sequence is human NY-ESO-1 protein. It is provided in a
CC specification relating to a method for determining the status of a
CC cancerous condition in a patient with a tumour that expresses NY-ESO-1.
CC The method comprises assaying a sample taken from the patient for
CC antibodies that specifically bind to the NY-ESO-1 and comparing the value
CC obtained to a prior value obtained from assay of a prior sample taken
CC from the patient. Any difference between the values is indicative of a
CC change in status of the cancerous condition. The method is useful for
CC determining whether a cancerous condition is progressing, regressing or
CC remaining stable, in particular in patients receiving treatment for a
CC melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
CC carcinoma
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 60; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 RASGPGGGAPR 11
              ||||||||||| 
Db         52 RASGPGGGAPR 62
```

Search completed: March 13, 2006, 19:04:00
Job time : 83.8235 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:04:24 ; Search time 13.0706 Seconds
(without alignments)
80.975 Million cell updates/sec

Title: US-09-529-206E-30
Perfect score: 60
Sequence: 1 RASGPGGGAPR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	44	73.3	3190	2	T13828	CREB-binding prote
2	42	70.0	351	2	S50754	hypothetical prote
3	42	70.0	378	2	C87425	aldose 1-epimerase
4	41	68.3	173	2	AB3648	flagellar basal-bo
5	41	68.3	286	2	S04673	H+-transporting tw
6	41	68.3	357	2	F82878	XAA-PRO aminopepti
7	41	68.3	1207	2	T00378	KIAA0641 protein -
8	40	66.7	335	2	S08341	myristylated alani
9	40	66.7	371	2	T39312	hypothetical prote
10	40	66.7	383	2	A86182	hypothetical prote
11	40	66.7	436	2	T36104	conserved hypothet
12	40	66.7	521	2	A29345	steroid hormone re
13	40	66.7	679	2	S02165	regulatory protein
14	40	66.7	954	2	A87431	regulatory protein
15	39	65.0	103	2	C72683	hypothetical prote
16	39	65.0	114	2	B45036	Pur beta - human (
17	39	65.0	163	2	E87464	competence/damage-
18	39	65.0	166	2	I69006	histocompatibility
19	39	65.0	187	2	T35619	hypothetical prote
20	39	65.0	260	2	F95899	probable transcrip
21	39	65.0	307	2	B72677	hypothetical prote
22	39	65.0	387	2	T52451	endopeptidase Clp
23	39	65.0	466	2	F95307	conserved hypothet
24	39	65.0	474	2	G75580	conserved hypothet
25	39	65.0	566	2	T34842	probable transfera
26	39	65.0	575	2	S35327	protein kinase sgg
27	39	65.0	620	2	T30765	hypothetical prote
28	39	65.0	627	2	T35608	polyketide hydroxy
29	39	65.0	733	2	S10932	probable protein k
30	39	65.0	743	2	C56695	transducin-like en
31	39	65.0	757	2	JC7726	(1->4)-alpha-D-glu
32	39	65.0	886	2	S07132	hypothetical prote
33	39	65.0	1028	2	A56038	DNA-binding protei
34	39	65.0	1067	2	S35423	protein kinase sgg
35	39	65.0	1213	2	S16356	ovo protein - frui
36	39	65.0	1317	2	T03748	apoptosis associat
37	39	65.0	4116	2	T13719	calo protein - fru
38	38	63.3	104	2	C72637	hypothetical prote
39	38	63.3	112	2	C87270	hypothetical prote
40	38	63.3	131	2	C75445	Pex-related protei
41	38	63.3	143	2	H87399	peptidyl-tRNA hydr
42	38	63.3	145	2	AH3506	peptidyl-tRNA hydr
43	38	63.3	161	2	S12246	anther-specific pr
44	38	63.3	185	2	T36874	hypothetical prote
45	38	63.3	189	2	AE3136	Hypothetical Prote

ALIGNMENTS

RESULT 1
T13828
CREB-binding protein homolog - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13828
R;Akimaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; G
Nature 386, 735-738, 1997
A;Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling
A;Reference number: Z17785; MUID:97263578; PMID:9109493
A;Accession: T13828
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3190 <AKI>
A;Cross-references: UNIPROT:O01368; UNIPARC:UPI000003EB83; EMBL:U88570; NID:g1916929; P
C;Genetics:
A;Cross-references: FlyBase:FBgn0015624
A;Map position: X
F;1723-1780/Domain: bromodomain homology <BRO>

Query Match 73.3%; Score 44; DB 2; Length 3190;
Best Local Similarity 77.8%; Pred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 SGPGGGAPR 11
              :||||| ||
Db        320 NGPGGGGPR 328
```

RESULT 2
S50754
hypothetical protein WP6 - Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S50754
R;Woessner, J.P.; Molendijk, A.J.; van Egmond, P.; Klis, F.M.; Goodenough, U.W.; Haring
Plant Mol. Biol. 26, 947-960, 1994
A;Title: Domain conservation in several volvocalean cell wall proteins.
A;Reference number: S50754; MUID:95093034; PMID:8000007
A;Accession: S50754
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-351 <WOE>
A;Cross-references: UNIPROT:Q39492; UNIPARC:UPI00000A170A; EMBL:L29028; NID:g530877; PI

Query Match 70.0%; Score 42; DB 2; Length 351;
Best Local Similarity 80.0%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 RASGPGGGAP 10
              ||| |||| |
Db        299 RASPPGGGPP 308
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RESULT 3
C87425
aldose 1-epimerase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: C87425
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87425
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-378 <STO>
A;Cross-references: UNIPROT:Q9A8D6; UNIPARC:UPI00000C73A0; GB:AE005673; NID:g13422779; P
C;Genetics:
A;Gene: CC1418
C;Superfamily: aldose 1-epimerase

  Query Match 70.0%; Score 42; DB 2; Length 378;
  Best Local Similarity 77.8%; Pred. No. 74;
  Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SGPGGGAPR 11
:|| |||||
Db 282 NGPSGGAPR 290

RESULT 4
AB3648
flagellar basal-body rod protein flgF [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AB3648
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AB3648
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <KUR>
A;Cross-references: UNIPROT:Q8YAZ4; UNIPARC:UPI0000058740; GB:AE008918; PIDN:AAL54349.1;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII1107
A;Map position: II

  Query Match 68.3%; Score 41; DB 2; Length 173;
  Best Local Similarity 100.0%; Pred. No. 53;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PGGGAPR 11
|||||||
Db 132 PGGGAPR 138

RESULT 5
S04673
H+-transporting two-sector ATPase (EC 3.6.3.14) gamma chain - Rhodopseudomonas blastica
C;Species: Rhodopseudomonas blastica
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 31-Dec-2004
C;Accession: S04673
R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A;Title: Rhodopseudomonas blastica atp operon. Nucleotide sequence and transcription.
A;Reference number: S04666; MUID:85058188; PMID:6209404
A;Accession: S04673
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-286 <TYB>
A;Cross-references: UNIPROT:P05436; UNIPARC:UPI0000126582
C;Superfamily: H(+)-transporting ATP synthase gamma chain
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

  Query Match 68.3%; Score 41; DB 2; Length 286;
  Best Local Similarity 80.0%; Pred. No. 81;
  Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ASGPGGGAPR 11
||| | ||||
Db 57 ASGQGAGAPR 66

RESULT 6
F82878
XAA-PRO aminopeptidase UU532 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: F82878
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mi
A;Reference number: A82870
A;Accession: F82878
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <GLA>
A;Cross-references: UNIPARC:UPI00000C1CAC; GB:AE002152; GB:AF222894; NID:g6899532; PIDN
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: pepP; UU532
A;Genetic code: SGC3
C;Superfamily: X-Pro aminopeptidase

  Query Match 68.3%; Score 41; DB 2; Length 357;
  Best Local Similarity 77.8%; Pred. No. 97;
  Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASGPGGGAP 10
|||| ||:|
Db 193 ASGPNGGSP 201

RESULT 7
T00378
KIAA0641 protein - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Accession: T00378
R;Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N
DNA Res. 5, 169-176, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. X. The complete
A;Reference number: Z14142; MUID:98403880; PMID:9734811
A;Accession: T00378
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1207 <ISH>
A;Cross-references: UNIPARC:UPI0000046CF7; EMBL:AB014541; NID:g3327095; PIDN:BAA31616.1,
C;Genetics:
A;Gene: KIAA0641

  Query Match 68.3%; Score 41; DB 2; Length 1207;
  Best Local Similarity 70.0%; Pred. No. 2.7e+02;
  Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ASGPGGGAPR 11
|:|| || ||
Db 757 ATGPSGGQPR 766

```
RESULT 8
S08341
myristylated alanine-rich protein kinase C substrate - bovine
N;Alternate names: acidic calmodulin-binding 81K protein (ACAMP-81); MARCKS
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S08341; A32904; S29270; A46098; PS0338
R;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
Nucleic Acids Res. 17, 3987-3988, 1989
A;Title: Nucleotide sequence of a cDNA for the bovine myristoylated alanine-rich C kinas
A;Reference number: S08341; MUID:89282412; PMID:2734111
A;Accession: S08341
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-335 <STU>
A;Cross-references: UNIPROT:P12624; UNIPARC:UPI000016C340; EMBL:M24638; NID:g163339; PID
R;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 4012-4016, 1989
A;Title: Molecular cloning, characterization, and expression of a cDNA encoding the "80-
A;Reference number: A32904; MUID:89264553; PMID:2726763
A;Accession: A32904
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-98,'Q',100-335 <ST2>
A;Cross-references: UNIPARC:UPI000017750A; GB:M24638; GB:M23738
R;Herget, T.; Brooks, S.F.; Broad, S.; Rozengurt, E.
Eur. J. Biochem. 209, 7-14, 1992
A;Title: Relationship between the major protein kinase C substrates acidic 80-kDa protei
 or equivalent genes in different species.
A;Reference number: S29267; MUID:93011168; PMID:1396720
A;Accession: S29270
A;Molecule type: DNA
A;Residues: 191-253,'SEE',257-279,283-292,'V',294,'PEQE',299,'A',300,'A',302-313,'A',315
A;Cross-references: UNIPARC:UPI000017750B
R;Manenti, S.; Sorokine, O.; Van Dorsselaer, A.; Taniguchi, H.
J. Biol. Chem. 268, 6878-6881, 1993
A;Title: Isolation of the non-myristoylated form of a major substrate of protein kinase
A;Reference number: A46098; MUID:93216617; PMID:8463217
A;Accession: A46098
A;Molecule type: protein
A;Residues: 2-11 <MAN>
A;Cross-references: UNIPARC:UPI000017750C
R;Mizutani, A.; Tokumitsu, H.; Hidaka, H.
Biochem. Biophys. Res. Commun. 182, 1395-1401, 1992
A;Title: Acidic calmodulin binding protein, ACAMP-81, is MARCKS protein interacting with
A;Reference number: PS0338; MUID:92171958; PMID:1540183
A;Accession: PS0338
A;Molecule type: protein
A;Residues: 12-30;56-69;88-98,'AS',100-103;104-109,'E',111-123;156-160;165-171;196-215;2
A;Cross-references: UNIPARC:UPI000017750D; UNIPARC:UPI000017750E; UNIPARC:UPI000017750F;
514
A;Experimental source: brain
A;Note: this sequence is identical with that of myristoylated alanine-rich C-kinase subs
C;Comment: This protein is a major cellular substrate for protein kinase C and plays a r
C;Comment: It binds to calmodulin in one to one molar ratio in the presence of calcium a
C;Genetics:
A;Introns: 34/3
C;Superfamily: neurofilament triplet H protein
C;Keywords: actin binding; blocked amino end; calmodulin binding; lipoprotein; myristyla
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;158,162,166,169/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status

  Query Match             66.7%;  Score 40;  DB 2;  Length 335;
  Best Local Similarity   64.3%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    4;  Gaps    1;

Qy          2 ASGPG----GGAPR 11
              |:|||    |||||
Db        288 AAGPGCPRAGGAPR 301


RESULT 9
T39312
hypothetical protein SPBC119.14 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39312
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, March 1998
A;Reference number: Z21843
A;Accession: T39312
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-371 <WOO>
A;Cross-references: UNIPROT:O42905; UNIPARC:UPI00001352D5; EMBL:AL022117; PIDN:CAA17929
A;Experimental source: strain 972h-; cosmid c119
C;Genetics:
A;Gene: SPDB:SPBC119.14
A;Map position: 2
A;Introns: 77/3; 105/3; 165/3; 250/1; 276/2

  Query Match             66.7%;  Score 40;  DB 2;  Length 371;
  Best Local Similarity   77.8%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGA 9
              | |||||||:
Db         36 RRSGPGGGS 44


RESULT 10
A86182
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86182
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86182
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-383 <STO>
A;Cross-references: UNIPROT:Q9MAT5; UNIPARC:UPI00000A6788; GB:AE005172; NID:g7211979; P
C;Genetics:
A;Map position: 1

  Query Match             66.7%;  Score 40;  DB 2;  Length 383;
  Best Local Similarity   70.0%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAP 10
              ||:| ||| |
Db         13 RAAGTGGGGP 22


RESULT 11
T36104
conserved hypothetical protein SCE15.01 - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36104
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1999
A;Reference number: Z21597
A;Accession: T36104
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Residues: 1-436 <MUR>
A;Cross-references: UNIPROT:Q8CJX1; UNIPARC:UPI000017AD99; EMBL:AL049707; PIDN:CAB41270.
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCE15.01

  Query Match             66.7%;  Score 40;  DB 2;  Length 436;
  Best Local Similarity   77.8%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 ASGPGGGAP 10
              ||||||  |
Db        153 ASGPGGNTP 161


RESULT 12
A29345
steroid hormone receptor ERR1 precursor - human
N;Alternate names: estrogen-related receptor
C;Species: Homo sapiens (man)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 31-Dec-2004
C;Accession: A29345; A49074
R;Giguere, V.; Yang, N.; Segui, P.; Evans, R.M.
Nature 331, 91-94, 1988
A;Title: Identification of a new class of steroid hormone receptors.
A;Reference number: A29345; MUID:88122546; PMID:3267207
A;Accession: A29345
A;Molecule type: mRNA
A;Residues: 1-521 <GIG>
A;Cross-references: UNIPROT:P11474; UNIPARC:UPI0000142399; EMBL:X51416; NID:g36608; PIDN
R;Wiley, S.R.; Kraus, R.J.; Zuo, F.; Murray, E.E.; Loritz, K.; Mertz, J.E.
Genes Dev. 7, 2206-2219, 1993
A;Title: SV40 early-to-late switch involves titration of cellular transcriptional repres
A;Reference number: A49074; MUID:94040741; PMID:8224847
A;Accession: A49074
A;Status: preliminary
A;Molecule type: protein
A;Residues: 166-169,'X',171-173 <WIL>
A;Cross-references: UNIPARC:UPI000017A1DF
C;Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zi
F;174-434/Domain: erbA transforming protein homology <ERBA>
F;176-196/Region: zinc finger
F;212-236/Region: zinc finger

  Query Match             66.7%;  Score 40;  DB 2;  Length 521;
  Best Local Similarity   77.8%;  Pred. No. 1.8e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 SGPGGGAPR 11
              :||||||  |
Db        465 AGPGGGAER 473


RESULT 13
S02165
regulatory protein flaY - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S02165
R;Kaplan, J.B.; Dingwall, A.; Bryan, R.; Champer, R.; Shapiro, L.
J. Mol. Biol. 205, 71-83, 1989
A;Title: Temporal regulation and overlap organization of two Caulobacter flagellar genes
A;Reference number: S02164; MUID:89178645; PMID:2648000
A;Accession: S02165
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-679 <KAP>
A;Cross-references: UNIPROT:P15345; UNIPARC:UPI000017A8F7
C;Genetics:
A;Gene: flaY
C;Keywords: transcription regulation

  Query Match             66.7%;  Score 40;  DB 2;  Length 679;
  Best Local Similarity   77.8%;  Pred. No. 2.3e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 ASGPGGGAP 10
              | |||  |||
Db        173 AGGPGAGAP 181


RESULT 14
A87431
regulatory protein FlaEY [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87431
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87431
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-954 <STO>
A;Cross-references: UNIPROT:P15345; UNIPARC:UPI000012A8ED; GB:AE005673; NID:g13422833; P
C;Genetics:
A;Gene: CC1465

  Query Match             66.7%;  Score 40;  DB 2;  Length 954;
  Best Local Similarity   77.8%;  Pred. No. 3.1e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 ASGPGGGAP 10
              | |||  |||
Db        317 AGGPGAGAP 325


RESULT 15
C72683
hypothetical protein APE0884 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: C72683
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: C72683
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-103 <KAW>
A;Cross-references: UNIPROT:Q9YDN0; UNIPARC:UPI000005DD18; DDBJ:AP000060; NID:g5104188;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0884

  Query Match             65.0%;  Score 39;  DB 2;  Length 103;
  Best Local Similarity   85.7%;  Pred. No. 66;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GPGGGAP 10
              |||||:|
Db         21 GPGGGSP 27


Search completed: March 13, 2006, 19:16:12
Job time : 14.0706 secs
```

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 18:53:23 ; Search time 79.8471 Seconds
(without alignments)
97.196 Million cell updates/sec

Title: US-09-529-206E-30
Perfect score: 60
Sequence: 1 RASGPGGGAPR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	60	100.0	142	2	Q9NY13_HUMAN	Q9ny13 homo sapien
2	60	100.0	180	1	CTG1B_HUMAN	P78358 homo sapien
3	60	100.0	180	2	Q7LBY4_HUMAN	Q7lby4 homo sapien
4	52	86.7	210	1	CTAG2_HUMAN	O75638 homo sapien
5	50	83.3	362	2	Q63QT8_BURPS	Q63qt8 burkholderi
6	50	83.3	362	2	Q62H22_BURMA	Q62h22 burkholderi
7	47	78.3	449	2	Q7F1E3_ORYSA	Q7f1e3 oryza sativ
8	47	78.3	895	2	Q4NUK4_9DELT	Q4nuk4 anaeromyxob
9	46	76.7	175	1	PACA_CHICK	P41534 g glucagon-
10	46	76.7	194	2	Q96BU2_HUMAN	Q96bu2 homo sapien
11	46	76.7	327	2	Q63HT9_BURPS	Q63ht9 burkholderi
12	46	76.7	330	2	Q629N3_BURMA	Q629n3 burkholderi
13	46	76.7	383	2	Q4TEG9_TETNG	Q4teg9 tetraodon n
14	46	76.7	708	2	Q5KJM5_CRYNE	Q5kjm5 cryptococcu
15	46	76.7	708	2	Q55WM1_CRYNE	Q55wm1 cryptococcu
16	46	76.7	788	2	Q4QQP8_HUMAN	Q4qqp8 homo sapien
17	46	76.7	896	2	Q96D18_HUMAN	Q96d18 homo sapien
18	46	76.7	1000	2	Q4FKF7_9TRYP	Q4fkf7 trypanosoma
19	46	76.7	1253	2	Q6DHV6_HUMAN	Q6dhv6 homo sapien
20	46	76.7	1430	2	Q9H7P9_HUMAN	Q9h7p9 homo sapien
21	45	75.0	309	2	Q63N33_BURPS	Q63n33 burkholderi
22	45	75.0	432	2	Q7L0R7_HUMAN	Q7l0r7 homo sapien
23	45	75.0	444	2	Q9UPQ2_HUMAN	Q9upq2 homo sapien
24	45	75.0	504	2	Q4NVJ7_9DELT	Q4nvj7 anaeromyxob
25	45	75.0	678	2	Q8NAC4_HUMAN	Q8nac4 homo sapien
26	45	75.0	1379	2	Q7QEK5_ANOGA	Q7qek5 anopheles g
27	45	75.0	2013	2	Q4NWX4_9DELT	Q4nwx4 anaeromyxob
28	44	73.3	159	2	Q4RBL9_TETNG	Q4rbl9 tetraodon n
29	44	73.3	164	2	Q9DW95_RCMVM	Q9dw95 rat cytomeg
30	44	73.3	262	2	Q5Z8E2_ORYSA	Q5z8e2 oryza sativ
31	44	73.3	262	2	Q4NUZ3_9DELT	Q4nuz3 anaeromyxob
32	44	73.3	271	2	Q4NAC6_9MICC	Q4nac6 arthrobacte
33	44	73.3	321	2	Q96S27_HUMAN	Q96s27 homo sapien
34	44	73.3	367	2	Q6AV33_ORYSA	Q6av33 oryza sativ
35	44	73.3	398	2	Q8N6H2_HUMAN	Q8n6h2 homo sapien
36	44	73.3	398	2	Q5SQU1_HUMAN	Q5squ1 homo sapien
37	44	73.3	399	2	Q8IVQ3_HUMAN	Q8ivq3 homo sapien
38	44	73.3	411	2	Q6ERQ1_ORYSA	Q6erq1 oryza sativ
39	44	73.3	492	2	Q7NWI2_CHRVO	Q7nwi2 chromobacte
40	44	73.3	559	2	Q8L680_ORYSA	Q8l680 oryza sativ
41	44	73.3	566	2	Q5SQT4_HUMAN	Q5sqt4 homo sapien
42	44	73.3	580	2	Q7Q0A9_ANOGA	Q7q0a9 anopheles g
43	44	73.3	584	2	Q5P6Z0_AZOSE	Q5p6z0 azoarcus sp
44	44	73.3	702	2	Q4NQW2_9DELT	Q4nqw2 anaeromyxob
45	44	73.3	867	2	Q94LD1_ORYSA	Q94ld1 oryza sativ

ALIGNMENTS

RESULT 1
Q9NY13_HUMAN
ID Q9NY13_HUMAN PRELIMINARY; PRT; 142 AA.
AC Q9NY13;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein LAGE-2 (Fragment).
GN Name=LAGE-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ275978; CAB76945.1; -; mRNA.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;

Query Match 100.0%; Score 60; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 RASGPGGGAPR 11
              ||||||||||
Db         26 RASGPGGGAPR 36
```

RESULT 2
CTG1B_HUMAN
ID CTG1B_HUMAN STANDARD; PRT; 180 AA.
AC P78358;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-
DE ESO-1).
GN Name=CTAG1B; Synonyms=CTAG, CTAG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
RA Chen Y.-T., Scanlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,
RA Williamson B., Stockert E., Pfreundschuh M., Old L.J.;
RT "A testicular antigen aberrantly expressed in human cancers detected
RT by autologous antibody screening.";

```
RL   Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Melanoma;
RX   MEDLINE=98289662; PubMed=9626360;
RA   Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA   de Plaen E., Boon T.;
RT   "LAGE-1, a new gene with tumor specificity.";
RL   Int. J. Cancer 76:903-908(1998).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98430682; PubMed=9759882;
RA   Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,
RA   Schwartzentruber D.J., Rosenberg S.A.;
RT   "A breast and melanoma-shared tumor antigen: T cell responses to
RT   antigenic peptides translated from different open reading frames.";
RL   J. Immunol. 161:3596-3606(1998).
CC   -!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide
CC       variety of cancers. Detected in uterine myometrium.
CC   -!- SIMILARITY: Belongs to the CTAG family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U87459; AAB49693.1; -; mRNA.
DR   EMBL; AJ003149; CAA05908.1; -; mRNA.
DR   EMBL; AF038567; AAD05202.1; -; mRNA.
DR   HGNC; HGNC:2491; CTAG1B.
DR   MIM; 300156; -.
KW   Antigen; Transmembrane.
FT   TRANSMEM    156    172       Potential.
FT   COMPBIAS       5     82       Gly-rich.
SQ   SEQUENCE   180 AA;  17992 MW;  B122C5C2C8BE1569 CRC64;

  Query Match             100.0%;  Score 60;  DB 1;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.49;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||| |
Db         52 RASGPGGGAPR 62


RESULT 3
Q7LBY4_HUMAN
ID   Q7LBY4_HUMAN PRELIMINARY;      PRT;   180 AA.
AC   Q7LBY4;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
DE   antigen 1-A).
GN   Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21303268;
RA   Galgoczy P., Rosenthal A., Platzer M.;
RT   "Human-mouse comparative sequence analysis of the NEMO gene reveals an
RT   alternative promoter within the neighboring G6PD gene.";
RL   Gene 271:93-98(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21566154; PubMed=11709543; DOI=10.1093/hmg/10.22.2557;
RA   Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
RA   Patlan H., Ciccodicola A., Kenwrick S., Platzer M., D'Urso M.,
RA   Nelson D.L.;
RT   "Multiple pathogenic and benign genomic rearrangements occur at a 35
RT   kb duplication involving the NEMO and LAGE2 genes.";
RL   Hum. Mol. Genet. 10:2557-2567(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Platzer M.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Platzer M.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RA   Galgoczy P., Platzer M.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99454989; PubMed=10523621;
RA   De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
RT   "DNA methylation is the primary silencing mechanism for a set of germ
RT   line- and tumor-specific genes with a CpG-rich promoter.";
RL   Mol. Cell. Biol. 19:7327-7335(1999).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RA   Lethe B.G.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF277315; AAL27014.1; -; Genomic_DNA.
DR   EMBL; AJ275977; CAB76943.1; -; Genomic_DNA.
DR   EMBL; AF277315; AAL27013.1; -; Genomic_DNA.
SQ   SEQUENCE   180 AA;  17992 MW;  B122C5C2C8BE1569 CRC64;

  Query Match             100.0%;  Score 60;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.49;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||| |
Db         52 RASGPGGGAPR 62


RESULT 4
CTAG2_HUMAN
ID   CTAG2_HUMAN    STANDARD;      PRT;   210 AA.
AC   O75638; O75637; Q9BU80; Q9UJ89; Q9Y479;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
GN   Name=CTAG2; Synonyms=ESO2, LAGE1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B).
RC   TISSUE=Melanoma;
RX   MEDLINE=98289662; PubMed=9626360;
RA   Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA   de Plaen E., Boon T.;
RT   "LAGE-1, a new gene with tumor specificity.";
RL   Int. J. Cancer 76:903-908(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B), AND VARIANTS
RP   GLN-6; GLN-89 AND ARG-138.
RC   TISSUE=Melanoma;
RX   MEDLINE=99325550; PubMed=10399963;
RA   Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT   "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT   unexpected translation product of LAGE-1.";
RL   Int. J. Cancer 82:442-448(1999).
RN   [3]
```

```
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
RP   ARG-138.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=LAGE-1B; Synonyms=LAGE-1L;
CC         IsoId=O75638-1; Sequence=Displayed;
CC       Name=LAGE-1A; Synonyms=LAGE-1S;
CC         IsoId=O75638-2; Sequence=VSP_004301;
CC   -!- TISSUE SPECIFICITY: Testis and very low level in placenta and in
CC       some uterus samples. Observed in 25-50% of tumor samples of
CC       melanomas, non-small-cell lung carcinomas, bladder, prostate and
CC       head and neck cancers.
CC   -!- DOMAIN: A transmembrane domain is present in isoform LAGE-1A.
CC   -!- SIMILARITY: Belongs to the CTAG family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AJ223093; CAA11117.1; -; Genomic_DNA.
DR   EMBL; AJ223093; CAA11116.1; -; Genomic_DNA.
DR   EMBL; AJ223040; CAA11043.1; -; mRNA.
DR   EMBL; AJ223041; CAA11044.1; -; mRNA.
DR   EMBL; AJ012834; CAA10194.1; -; mRNA.
DR   EMBL; AJ012835; CAA10196.1; -; mRNA.
DR   EMBL; BC002833; AAH02833.1; -; mRNA.
DR   Ensembl; ENSG00000126890; Homo sapiens.
DR   HGNC; HGNC:2492; CTAG2.
DR   H-InvDB; HIX0017163; -.
DR   MIM; 300396; -.
KW   Alternative splicing; Antigen; Polymorphism; Transmembrane.
FT   COMPBIAS      5     79       Gly-rich.
FT   COMPBIAS    183    188       Poly-Pro.
FT   VARSPLIC    135    210       MSVWDQDREGAGRMRVVGWGLGSASPEGQKARDLRTPKHKV
FT                                SEQRPGTPGPPPPEGAQGDGCRGVAFNVMFSAPHI -> IR
FT                                LTAADHRQLQLSISSCLQQLSLLMWITQCFLPVFLAQAPSG
FT                                QRR (in isoform LAGE-1A).
FT                                /FTId=VSP_004301.
FT   VARIANT       6      6       R -> Q.
FT                                /FTId=VAR_007855.
FT   VARIANT      89     89       E -> Q.
FT                                /FTId=VAR_007856.
FT   VARIANT     138    138       W -> R.
FT                                /FTId=VAR_007857.
SQ   SEQUENCE   210 AA;  21120 MW;  8BE0EE00AE55E8BE CRC64;

  Query Match             86.7%;  Score 52;  DB 1;  Length 210;
  Best Local Similarity   90.9%;  Pred. No. 8.3;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||| |||||
Db         52 RASGPRGGAPR 62


RESULT 5
Q63QT8_BURPS
ID   Q63QT8_BURPS PRELIMINARY;      PRT;   362 AA.
AC   Q63QT8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative DNA polymerase III.
GN   OrderedLocusNames=BPSL2936;
OS   Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia; pseudomallei group.
OX   NCBI_TaxID=28450;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=K96243;
RX   PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA   Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
RA   Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA   Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
RA   Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA   Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D.,
RA   Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA   Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA   Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA   Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA   Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT   "Genomic plasticity of the causative agent of melioidosis,
RT   Burkholderia pseudomallei.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR   EMBL; BX571965; CAH36946.1; -; Genomic_DNA.
DR   GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR   GO; GO:0006260; P:DNA replication; IEA.
DR   InterPro; IPR010372; DNA_pol3_delta.
DR   InterPro; IPR005790; DNA_polIII_delta.
DR   Pfam; PF06144; DNA_pol3_delta; 1.
DR   TIGRFAMs; TIGR01128; holA; 1.
KW   Complete proteome.
SQ   SEQUENCE   362 AA;  38726 MW;  D5FF3DE783D41E41 CRC64;

  Query Match             83.3%;  Score 50;  DB 2;  Length 362;
  Best Local Similarity   81.8%;  Pred. No. 28;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||:|||| |||
Db        349 RAAGPGGDAPR 359


RESULT 6
Q62H22_BURMA
ID   Q62H22_BURMA PRELIMINARY;      PRT;   362 AA.
AC   Q62H22;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   DNA polymerase III, delta subunit (EC 2.7.7.7).
GN   Name=holA; OrderedLocusNames=BMA2451;
OS   Burkholderia mallei (Pseudomonas mallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia.
OX   NCBI_TaxID=13373;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ATCC 23344;
RX   PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA   Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
```

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RA   Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA   Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA   Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA   Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
RA   Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA   Zafar N., Zhou L., Fraser C.M.;
RT   "Structural flexibility in the Burkholderia mallei genome.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR   EMBL; CP000010; AAU49707.1; -; Genomic_DNA.
DR   TIGR; BMA2451; -.
DR   GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006260; P:DNA replication; IEA.
DR   InterPro; IPR010372; DNA_pol3_delta.
DR   InterPro; IPR005790; DNA_polIII_delta.
DR   Pfam; PF06144; DNA_pol3_delta; 1.
DR   TIGRFAMs; TIGR01128; holA; 1.
KW   Complete proteome; Nucleotidyltransferase; Transferase.
SQ   SEQUENCE   362 AA;  38726 MW;  D5FF3DE783D41E41 CRC64;

  Query Match             83.3%;  Score 50;  DB 2;  Length 362;
  Best Local Similarity   81.8%;  Pred. No. 28;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||:|||| |||
Db        349 RAAGPGGDAPR 359


RESULT 7
Q7F1E3_ORYSA
ID   Q7F1E3_ORYSA PRELIMINARY;      PRT;   449 AA.
AC   Q7F1E3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Hypothetical protein OJ1191_A10.131 (Hypothetical protein
DE   OJ1014_E06.5).
GN   Name=OJ1191_A10.131; Synonyms=OJ1014_E06.5;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR   EMBL; AP003857; BAD08744.1; -; Genomic_DNA.
DR   EMBL; AP003888; BAD11573.1; -; Genomic_DNA.
DR   Gramene; Q7F1E3; -.
DR   GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0016567; P:protein ubiquitination; IEA.
DR   InterPro; IPR008700; NOI.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF05627; NOI; 1.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ   SEQUENCE   449 AA;  47196 MW;  B8EFF7708B292296 CRC64;

  Query Match             78.3%;  Score 47;  DB 2;  Length 449;
  Best Local Similarity   81.8%;  Pred. No. 94;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              || | ||||||
Db        157 RAKGGGGGAPR 167


RESULT 8
Q4NUK4_9DELT
ID   Q4NUK4_9DELT PRELIMINARY;      PRT;   895 AA.
AC   Q4NUK4;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   LigA.
GN   ORFNames=AdehDRAFT_2813;
OS   Anaeromyxobacter dehalogenans 2CP-C.
OC   Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC   Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
OX   NCBI_TaxID=290397;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=2CP-C;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome assembly of Anaeromyxobacter
RT   dehalogenans 2CP-C.";
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=2CP-C;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Anaeromyxobacter
RT   dehalogenans 2CP-C.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAHD01000013; EAL79351.1; -; Genomic_DNA.
SQ   SEQUENCE   895 AA;  93871 MW;  0AE25BBBF172BDB0 CRC64;

  Query Match             78.3%;  Score 47;  DB 2;  Length 895;
  Best Local Similarity   81.8%;  Pred. No. 1.8e+02;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              || | ||||||
Db        799 RARGAGGGAPR 809


RESULT 9
PACA_CHICK
ID   PACA_CHICK     STANDARD;      PRT;   175 AA.
AC   P41534; Q53WW0;
DT   01-NOV-1995 (Rel. 32, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Glucagon-family neuropeptides precursor [Contains: Growth hormone-
DE   releasing factor 1-46 (GRF) (Growth hormone-releasing hormone) (GHRH);
DE   Pituitary adenylate cyclase activating polypeptide-27 (PACAP-27)
DE   (PACAP27); Pituitary adenylate cyclase activating polypeptide-38
DE   (PACAP-38) (PACAP38)].
GN   Name=ADCYAP1;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].
RX   MEDLINE=97174314; PubMed=9022048;
RA   McRory J.E., Parker R.L., Sherwood N.M.;
RT   "Expression and alternative processing of a chicken gene encoding both
RT   growth hormone-releasing hormone and pituitary adenylate cyclase-
RT   activating polypeptide.";
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RL   DNA Cell Biol. 16:95-102(1997).
RN   [2]
RP   PROTEIN SEQUENCE OF 131-168.
RA   Yasuhara T., Mizuno K., Somogyvari-Vigh A., Komaki G., Arimura A.;
RT   "Isolation and primary structure of chicken PACAP.";
RL   Regul. Pept. 37:326-326(1992).
CC   -!- FUNCTION: Primary role of GRF is to release GH from the pituitary.
CC   -!- FUNCTION: PACAP plays pivotal roles as a neurotransmitter and/or a
CC       neuromodulator.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=GRF 1-46;
CC         IsoId=P41534-1; Sequence=Displayed;
CC       Name=GRF 1-43;
CC         IsoId=P41534-2; Sequence=VSP_001760;
CC       Name=GRF 33-46;
CC         IsoId=P41534-3; Sequence=VSP_001759;
CC   -!- SIMILARITY: Belongs to the glucagon family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U71183; AAB51200.1; -; mRNA.
DR   EMBL; U71184; AAB51201.1; -; mRNA.
DR   EMBL; U71185; AAB51202.1; -; mRNA.
DR   EMBL; U67275; AAC64494.1; -; Genomic_DNA.
DR   HSSP; P18509; 1GEA.
DR   InterPro; IPR000532; Glucagon.
DR   Pfam; PF00123; Hormone_2; 2.
DR   PRINTS; PR00275; GLUCAGON.
DR   PROSITE; PS00260; GLUCAGON; 2.
KW   Alternative splicing; Amidation; Cleavage on pair of basic residues;
KW   Direct protein sequencing; Glucagon family; Hormone; Signal.
FT   SIGNAL       1     23       Potential.
FT   PROPEP       24    80
FT   PEPTIDE      83    128      Growth hormone-releasing factor 1-46.
FT   PEPTIDE      131   168      Pituitary adenylate cyclase activating
FT                               polypeptide-38.
FT   PEPTIDE      131   157      Pituitary adenylate cyclase activating
FT                               polypeptide-27.
FT   PROPEP       172   175
FT   MOD_RES      157   157      Leucine amide (G-158 provides amide
FT                               group).
FT   MOD_RES      168   168      Lysine amide (G-169 provides amide
FT                               group).
FT   VARSPLIC     82    114      RHADGIFSKAYRKLLGQLSARNYLHSLMAKRVG -> S
FT                               (in isoform GRF 33-46).
FT                               /FTId=VSP_001759.
FT   VARSPLIC     115   117      Missing (in isoform GRF 1-43).
FT                               /FTId=VSP_001760.
SQ   SEQUENCE   175 AA;  19561 MW;  0DB54995F0AA9DFB CRC64;

  Query Match             76.7%;  Score 46;  DB 1;  Length 175;
  Best Local Similarity   72.7%;  Pred. No. 52;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||  |||| ||
Db         56 RAGAPGGGGPR 66


RESULT 10
Q96BU2_HUMAN
ID   Q96BU2_HUMAN PRELIMINARY;      PRT;   194 AA.
AC   Q96BU2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   PLEKHG2 protein (Fragment).
GN   Name=PLEKHG2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pancreas;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pancreas;
RA   Director MGC Project;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC015174; AAH15174.1; -; mRNA.
FT   NON_TER      1     1
SQ   SEQUENCE   194 AA;  19957 MW;  91AB4FF8F05CBD3C CRC64;

  Query Match             76.7%;  Score 46;  DB 2;  Length 194;
  Best Local Similarity   80.0%;  Pred. No. 58;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAP 10
              |  ||||||
Db        100 RRQGPGGGAP 109


RESULT 11
Q63HT9_BURPS
ID   Q63HT9_BURPS PRELIMINARY;      PRT;   327 AA.
AC   Q63HT9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative lipoprotein.
GN   OrderedLocusNames=BPSS2331;
OS   Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia; pseudomallei group.
OX   NCBI_TaxID=28450;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=K96243;
RX   PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA   Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
RA   Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA   Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
RA   Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA   Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D.,
RA   Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA   Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA   Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
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RA   Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA   Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT   "Genomic plasticity of the causative agent of melioidosis,
RT   Burkholderia pseudomallei.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR   EMBL; BX571966; CAH39817.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR007428; VacJ.
DR   Pfam; PF04333; VacJ; 1.
DR   PRINTS; PR01805; VACJLIPOPROT.
KW   Complete proteome; Lipoprotein.
SQ   SEQUENCE   327 AA;  33687 MW;  AC5D2C7CC4A44A25 CRC64;

  Query Match             76.7%;  Score 46;  DB 2;  Length 327;
  Best Local Similarity   88.9%;  Pred. No. 96;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ASGPGGGAP 10
              | |||||||
Db        243 AGGPGGGAP 251


RESULT 12
Q629N3_BURMA
ID   Q629N3_BURMA PRELIMINARY;      PRT;   330 AA.
AC   Q629N3;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative lipoprotein.
GN   OrderedLocusNames=BMAA2092;
OS   Burkholderia mallei (Pseudomonas mallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia.
OX   NCBI_TaxID=13373;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ATCC 23344;
RX   PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA   Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA   Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA   Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA   Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA   Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
RA   Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA   Zafar N., Zhou L., Fraser C.M.;
RT   "Structural flexibility in the Burkholderia mallei genome.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR   EMBL; CP000011; AAU47030.1; -; Genomic_DNA.
DR   TIGR; BMAA2092; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR007428; VacJ.
DR   Pfam; PF04333; VacJ; 1.
DR   PRINTS; PR01805; VACJLIPOPROT.
KW   Complete proteome; Lipoprotein.
SQ   SEQUENCE   330 AA;  33977 MW;  2F12165CD7366835 CRC64;

  Query Match             76.7%;  Score 46;  DB 2;  Length 330;
  Best Local Similarity   88.9%;  Pred. No. 97;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ASGPGGGAP 10
              | |||||||
Db        243 AGGPGGGAP 251


RESULT 13
Q4TEG9_TETNG
ID   Q4TEG9_TETNG PRELIMINARY;      PRT;   383 AA.
AC   Q4TEG9;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome undetermined SCAF5395, whole genome shotgun sequence.
DE   (Fragment).
GN   ORFNames=GSTENG00002257001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01005395; CAF88713.1; -; Genomic_DNA.
FT   NON_TER       1       1
SQ   SEQUENCE   383 AA;  39582 MW;  A61F4ECF2EEC3861 CRC64;

  Query Match             76.7%;  Score 46;  DB 2;  Length 383;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAP 10
              |  |||||||
Db        168 RPQGPGGGAP 177


RESULT 14
Q5KJM5_CRYNE
ID   Q5KJM5_CRYNE PRELIMINARY;      PRT;   708 AA.
AC   Q5KJM5;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Actin cross-linking, putative.
GN   ORFNames=CNC06000;
OS   Cryptococcus neoformans var. neoformans JEC21.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC   Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX   NCBI_TaxID=214684;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=JEC21;
RA   Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,
RA   Van Aken S., Fraser C.;
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=JEC21;
RX   PubMed=15653466; DOI=10.1126/science.1103773;
RA   Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
RA   Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
RA   Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
RA   D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
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RA   Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
RA   Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,
RA   Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L.,
RA   Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA   Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
RA   Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
RA   Fraser C.M., Hyman R.W.;
RT   "The genome of the basidiomycetous yeast and human pathogen
RT   Cryptococcus neoformans.";
RL   Science 307:1321-1324(2005).
DR   EMBL; AE017343; AAW42672.1; -; Genomic_DNA.
DR   GO; GO:0003779; F:actin binding; IEA.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   InterPro; IPR001589; Actnin_actin_bd.
DR   InterPro; IPR001715; Calponin_act_bd.
DR   InterPro; IPR011992; EF-Hand_type.
DR   InterPro; IPR002017; Spectrin.
DR   Pfam; PF00307; CH; 2.
DR   SMART; SM00033; CH; 2.
DR   PROSITE; PS00019; ACTININ_1; UNKNOWN_1.
DR   PROSITE; PS00020; ACTININ_2; 1.
DR   PROSITE; PS50021; CH; 2.
KW   Complete proteome.
SQ   SEQUENCE   708 AA;  79873 MW;  BAF52D1DD2C99B9D CRC64;

  Query Match             76.7%;  Score 46;  DB 2;  Length 708;
  Best Local Similarity   88.9%;  Pred. No. 2.1e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ASGPGGGAP 10
              | |||||||
Db         47 AGGPGGGAP 55


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ID   Q55WM1_CRYNE PRELIMINARY;      PRT;   708 AA.
AC   Q55WM1;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=CNBC1180;
OS   Cryptococcus neoformans var. neoformans B-3501A.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC   Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX   NCBI_TaxID=283643;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=B-3501A;
RA   Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
RA   Wickes B.L., Fu J., Davis R.W.;
RT   "Cryptococcus neoformans serotype D sequencing.";
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAEY01000013; EAL21978.1; -; Genomic_DNA.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   InterPro; IPR001589; Actnin_actin_bd.
DR   InterPro; IPR001715; Calponin_act_bd.
DR   InterPro; IPR011992; EF-Hand_type.
DR   InterPro; IPR002017; Spectrin.
DR   Pfam; PF00307; CH; 2.
DR   SMART; SM00033; CH; 2.
DR   PROSITE; PS00019; ACTININ_1; UNKNOWN_1.
DR   PROSITE; PS00020; ACTININ_2; UNKNOWN_1.
DR   PROSITE; PS50021; CH; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   708 AA;  79873 MW;  BAF52D1DD2C99B9D CRC64;

  Query Match             76.7%;  Score 46;  DB 2;  Length 708;
  Best Local Similarity   88.9%;  Pred. No. 2.1e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ASGPGGGAP 10
              | |||||||
Db         47 AGGPGGGAP 55


Search completed: March 13, 2006, 19:14:29
Job time : 80.8471 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:14:49 ; Search time 20.4471 Seconds
(without alignments)
44.477 Million cell updates/sec

Title: US-09-529-206E-30
Perfect score: 60
Sequence: 1 RASGPGGGAPR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	60	100.0	180	1	US-08-791-495-9	Sequence 9, Appli
2	60	100.0	180	2	US-08-937-263B-8	Sequence 8, Appli
3	60	100.0	180	2	US-09-751-798-8	Sequence 8, Appli
4	60	100.0	180	2	US-09-392-714-25	Sequence 25, Appl
5	60	100.0	180	2	US-09-165-546D-15	Sequence 15, Appl
6	60	100.0	180	2	US-09-341-829A-9	Sequence 9, Appli
7	60	100.0	180	2	US-09-849-602-30	Sequence 30, Appl
8	52	86.7	180	1	US-08-791-495-7	Sequence 7, Appli
9	52	86.7	180	2	US-09-341-829A-7	Sequence 7, Appli
10	52	86.7	210	1	US-08-791-495-5	Sequence 5, Appli
11	52	86.7	210	2	US-09-341-829A-5	Sequence 5, Appli
12	48	80.0	9	2	US-09-344-040C-117	Sequence 117, App
13	48	80.0	9	2	US-09-833-039A-117	Sequence 117, App
14	48	80.0	809	2	US-09-252-991A-31759	Sequence 31759, A
15	46	76.7	143	2	US-08-789-329C-10	Sequence 10, Appl
16	46	76.7	160	2	US-09-252-991A-17249	Sequence 17249, A
17	46	76.7	172	2	US-08-789-329C-7	Sequence 7, Appli
18	46	76.7	175	2	US-08-789-329C-3	Sequence 3, Appli
19	45	75.0	421	2	US-09-252-991A-32326	Sequence 32326, A
20	45	75.0	678	2	US-10-104-047-3295	Sequence 3295, Ap
21	45	75.0	1427	2	US-09-252-991A-20577	Sequence 20577, A
22	44	73.3	196	2	US-09-252-991A-30527	Sequence 30527, A
23	44	73.3	456	2	US-09-252-991A-17335	Sequence 17335, A
24	43	71.7	210	2	US-09-252-991A-24923	Sequence 24923, A
25	43	71.7	1228	2	US-09-252-991A-17764	Sequence 17764, A
26	42	70.0	283	2	US-09-252-991A-17831	Sequence 17831, A
27	42	70.0	836	2	US-09-491-356C-21	Sequence 21, Appl
28	41	68.3	177	2	US-09-252-991A-18782	Sequence 18782, A
29	41	68.3	310	2	US-09-252-991A-19986	Sequence 19986, A
30	41	68.3	340	2	US-09-949-002-562	Sequence 562, App
31	41	68.3	412	1	US-08-878-989-6	Sequence 6, Appli
32	41	68.3	412	2	US-09-272-796-6	Sequence 6, Appli
33	41	68.3	416	2	US-09-252-991A-30219	Sequence 30219, A
34	41	68.3	536	2	US-09-270-767-43766	Sequence 43766, A
35	41	68.3	555	2	US-10-104-047-3369	Sequence 3369, Ap
36	41	68.3	563	2	US-09-252-991A-17549	Sequence 17549, A
37	41	68.3	679	2	US-09-252-991A-27111	Sequence 27111, A
38	41	68.3	807	2	US-09-252-991A-32992	Sequence 32992, A
39	41	68.3	1000	2	US-09-252-991A-31361	Sequence 31361, A
40	41	68.3	1207	2	US-10-098-600B-16	Sequence 16, Appl
41	41	68.3	1207	2	US-09-949-002-376	Sequence 376, App
42	41	68.3	1323	2	US-09-248-796A-19543	Sequence 19543, A
43	41	68.3	1384	2	US-08-976-255-11	Sequence 11, Appl
44	40	66.7	137	2	US-09-252-991A-20489	Sequence 20489, A
45	40	66.7	174	2	US-09-902-540-12423	Sequence 12423, A

ALIGNMENTS

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RESULT 1
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL-1 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-791-495-9

  Query Match             100.0%;  Score 60;  DB 1;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.69;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
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Db         52 RASGPGGGAPR 62
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RESULT 2
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
;  GENERAL INFORMATION:
;    APPLICANT:  Chen, Yao-Tseng; Scanlan, Matthew;
;    APPLICANT:  Gure, Ali; Old, Lloyd J.; Jager, Elke;
;    APPLICANT:  Alexander, Knuth; Drijfhout, Jan W.
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULE
;    TITLE OF INVENTION:  ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
;    TITLE OF INVENTION:  ITSELF, AND USES THEREOF
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/937,263B
;      FILING DATE:  September 15, 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sinn, Eric, Patent Agent
;      REGISTRATION NUMBER:  40,177
;      REFERENCE/DOCKET NUMBER:  LUD 5466.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3000
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-937-263B-8

  Query Match             100.0%;  Score 60;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.69;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||||
Db         52 RASGPGGGAPR 62


RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
;  GENERAL INFORMATION:
;    APPLICANT:  Stockert, Elisabeth; Jager, Elke;
;    APPLICANT:  Chen, Yao-tseng; Scanlan, Matthew;
;    APPLICANT:  Knuth, Alexander; Old, Lloyd J.
;    TITLE OF INVENTION:  Antibodies Which Bind to NY-ESO-1 Cancer
;    TITLE OF INVENTION:  Associated Proteins, Uses Thereof,
;    TITLE OF INVENTION:  Truncated Forms of NY-ESO-1, and HLA
;    TITLE OF INVENTION:  Binding Peptides Derived Therefrom
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/751,798
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/062,422
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 6525177man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3168
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-09-751-798-8

  Query Match             100.0%;  Score 60;  DB 2;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 0.69;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||||
Db         52 RASGPGGGAPR 62


RESULT 4
US-09-392-714-25
; Sequence 25, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT: Gure, Ali O.
;  APPLICANT: Williamson, Barbara
;  APPLICANT: Chen, Yao-Tseng
;  APPLICANT: Old, Lloyd J.
;  TITLE OF INVENTION: Cancer Associated Antigens and Uses
;  TITLE OF INVENTION: Therefor
;  FILE REFERENCE: L0461/7062
;  CURRENT APPLICATION NUMBER: US/09/392,714A
;  CURRENT FILING DATE: 1999-09-09
;  EARLIER APPLICATION NUMBER: PCT/US98/14679
;  EARLIER FILING DATE: 1998-07-15
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-392-714-25

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  Best Local Similarity   100.0%;  Pred. No. 0.69;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||||
Db         52 RASGPGGGAPR 62
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; Sequence 15, Application US/09165546D
; Patent No. 6723832
;   GENERAL INFORMATION:
;        APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
;                   Gure, Ali, Old, Lloyd, Ritter, Gerd
;        TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                            SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
;                            USES THEREOF
;        NUMBER OF SEQUENCES: 15
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FULBRIGHT & JAWORSKI LLP
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10158
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/165,546D
;             FILING DATE: 02-Oct-1998
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: April 17, 1998
;             APPLICATION NUMBER: 08/937,263
;             FILING DATE: September 15, 1997
;             APPLICATION NUMBER: US 08/725,182
;             FILING DATE: October 3, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, No. 6723832man D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3000
;             TELEFAX: (212) 318-3400
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 180 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15

  Query Match           100.0%;  Score 60;  DB 2;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.69;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||
Db         52 RASGPGGGAPR 62


RESULT 6
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-9

  Query Match           100.0%;  Score 60;  DB 2;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 0.69;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||
Db         52 RASGPGGGAPR 62


RESULT 7
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; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT:  Old, Lloyd J.
;  APPLICANT:  Stockert, Elisabeth
;  APPLICANT:  Chen, Yao-Tseng
;  TITLE OF INVENTION: Colon Cancer Antigen Panel
;  FILE REFERENCE: L0461/7105(JRV)
;  CURRENT APPLICATION NUMBER: US/09/849,602
;  CURRENT FILING DATE:  2001-05-04
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-849-602-30

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Qy          1 RASGPGGGAPR 11
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Db         52 RASGPGGGAPR 62


RESULT 8
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL-1 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-791-495-7

  Query Match          86.7%;  Score 52;  DB 1;  Length 180;
  Best Local Similarity   90.9%;  Pred. No. 7.5;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
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Db         52 RASGPRGGAPR 62


RESULT 9
US-09-341-829A-7
; Sequence 7, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-7

  Query Match          86.7%;  Score 52;  DB 2;  Length 180;
  Best Local Similarity   90.9%;  Pred. No. 7.5;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||| |||||
Db         52 RASGPRGGAPR 62


RESULT 10
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL-1 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  210 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-791-495-5

  Query Match          86.7%;  Score 52;  DB 1;  Length 210;
  Best Local Similarity   90.9%;  Pred. No. 8.6;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||| |||||
Db         52 RASGPRGGAPR 62


RESULT 11
US-09-341-829A-5
; Sequence 5, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
;  APPLICANT: Leth,, Bernard
;  APPLICANT:  Lucas, Sophie
;  APPLICANT:  De Smet, Charles
;  APPLICANT:  Godelaine, Daniele
;  APPLICANT:  Boon-Falleur, Thierry
;  TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
;  FILE REFERENCE: L0461/7066
;  CURRENT APPLICATION NUMBER: US/09/341,829A
;  CURRENT FILING DATE:  1999-10-18
;  PRIOR APPLICATION NUMBER: US 08/791,495       <151> 1997-01-27
;  PRIOR APPLICATION NUMBER: PCT/US98/01445       <151> 1998-01-27
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-341-829A-5

  Query Match          86.7%;  Score 52;  DB 2;  Length 210;
  Best Local Similarity   90.9%;  Pred. No. 8.6;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||| |||||
Db         52 RASGPRGGAPR 62


RESULT 12
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US-09-344-040C-117
; Sequence 117, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
;  APPLICANT: Tureci, Ozlem
;  APPLICANT:  Sahin, Ugur
;  APPLICANT:  Pfreundschuh, Michael
;  APPLICANT:  Ramensee, Hans Georg
;  APPLICANT:  Stevanovic, Stefan
;  TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
;  TITLE OF INVENTION:  Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
;  TITLE OF INVENTION:  Gene, and Uses Thereof
;  FILE REFERENCE: LUD 5556.1
;  CURRENT APPLICATION NUMBER: US/09/344,040C
;  CURRENT FILING DATE:  1999-06-25
;  PRIOR APPLICATION NUMBER: US 09/105,839
;  PRIOR FILING DATE: 1998-06-26
;  PRIOR APPLICATION NUMBER: US 08/851,130
;  PRIOR FILING DATE: 1997-05-05
;  NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 117
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-344-040C-117

  Query Match             80.0%;  Score 48;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGA 9
              |||||||||
Db          1 RASGPGGGA 9


RESULT 13
US-09-833-039A-117
; Sequence 117, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
;  APPLICANT: Tureci, Ozlem
;  APPLICANT:  Sahin, Ugur
;  APPLICANT:  Pfreundschuh, Michael
;  TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
;  FILE REFERENCE: LUD 5622.1
;  CURRENT APPLICATION NUMBER: US/09/833,039A
;  CURRENT FILING DATE:  2001-04-12
;  PRIOR APPLICATION NUMBER: US 09/409,455
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: US 09/344,040
;  PRIOR FILING DATE: 1999-06-26
;  PRIOR APPLICATION NUMBER: US 09/105,839
;  PRIOR FILING DATE: 1998-06-26
;  NUMBER OF SEQ ID NOS: 131
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 117
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-833-039A-117

  Query Match             80.0%;  Score 48;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGA 9
              |||||||||
Db          1 RASGPGGGA 9


RESULT 14
US-09-252-991A-31759
; Sequence 31759, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 31759
;   LENGTH: 809
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31759

  Query Match             80.0%;  Score 48;  DB 2;  Length 809;
  Best Local Similarity   81.8%;  Pred. No. 93;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              || || |||||
Db        244 RAGGPRGGAPR 254


RESULT 15
US-08-789-329C-10
; Sequence 10, Application US/08789329C
; Patent No. 6165755
;  GENERAL INFORMATION:
;    APPLICANT:  SHERWOOD ET AL.
;    TITLE OF INVENTION:  CHICKEN NEUROPEPTIDE GENE USEFUL
;    TITLE OF INVENTION:  FOR IMPROVED POULTRY PRODUCTION
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klarquist Sparkman Campbell Leigh &
;      ADDRESSEE:  Whinston, LLP
;      STREET:  One World Trade Center
;      STREET:  121 S.W. Salmon Street
;      STREET:  Suite 1600
;      CITY:  Portland
;      STATE:  Oregon
;      COUNTRY:  United States of America
;      ZIP:  97204-2988
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Disk, 3-1/2 inch
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows NT
;      SOFTWARE:  WordPerfect 7.0 & ASCII
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/789,329C
;      FILING DATE:  01/23/97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Earp, David J.
;      REGISTRATION NUMBER:  41,401
;      REFERENCE/DOCKET NUMBER:  2847-46468/DJE
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (503) 226-7391
;      TELEFAX:  (503) 228-9446
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  143 aa
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-789-329C-10
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Query Match 76.7%; Score 46; DB 2; Length 143;
Best Local Similarity 72.7%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 RASGPGGGAPR 11
              ||  |||| ||
Db         56 RAGAPGGGGPR 66
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Search completed: March 13, 2006, 19:18:52
Job time : 20.4471 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:51:56 ; Search time 66.5176 Seconds
(without alignments)
69.096 Million cell updates/sec

Title: US-09-529-206E-30
Perfect score: 60
Sequence: 1 RASGPGGGAPR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	60	100.0	30	4	US-10-296-734-1404	Sequence 1404, Ap
2	60	100.0	179	5	US-10-482-029-202	Sequence 202, App
3	60	100.0	180	3	US-09-751-798-8	Sequence 8, Appli
4	60	100.0	180	3	US-09-849-602-30	Sequence 30, Appl
5	60	100.0	180	4	US-10-023-182-8	Sequence 8, Appli
6	60	100.0	180	4	US-10-207-655-71	Sequence 71, Appl
7	60	100.0	180	4	US-10-364-614-14	Sequence 14, Appl
8	60	100.0	180	4	US-10-026-066-3	Sequence 3, Appli
9	60	100.0	180	4	US-10-117-937-74	Sequence 74, Appl
10	60	100.0	180	4	US-10-295-027-386	Sequence 386, App
11	60	100.0	180	4	US-10-296-734-832	Sequence 832, App
12	60	100.0	180	4	US-10-188-832-139	Sequence 139, App
13	60	100.0	180	4	US-10-777-053-11	Sequence 11, Appl
14	60	100.0	180	4	US-10-751-088-15	Sequence 15, Appl
15	60	100.0	180	4	US-10-657-022-74	Sequence 74, Appl
16	60	100.0	180	4	US-10-837-217-11	Sequence 11, Appl
17	60	100.0	180	5	US-10-877-373-9	Sequence 9, Appli
18	60	100.0	180	5	US-10-723-860-1270	Sequence 1270, Ap
19	60	100.0	180	5	US-10-871-708-7	Sequence 7, Appli
20	60	100.0	180	5	US-10-895-523-3	Sequence 3, Appli
21	60	100.0	180	5	US-10-182-506A-3	Sequence 3, Appli
22	60	100.0	180	5	US-10-756-149-5024	Sequence 5024, Ap
23	60	100.0	180	6	US-11-067-064-74	Sequence 74, Appl
24	60	100.0	180	6	US-11-067-159-74	Sequence 74, Appl
25	60	100.0	397	3	US-09-821-883-27	Sequence 27, Appl
26	60	100.0	397	6	US-11-144-912-27	Sequence 27, Appl
27	60	100.0	3541	4	US-10-296-734-1454	Sequence 1454, Ap
28	55	91.7	10	4	US-10-447-161-39	Sequence 39, Appl
29	55	91.7	10	4	US-10-415-841A-52	Sequence 52, Appl
30	55	91.7	10	5	US-10-182-506A-23	Sequence 23, Appl
31	52	86.7	30	4	US-10-296-734-1436	Sequence 1436, Ap
32	52	86.7	135	4	US-10-295-027-388	Sequence 388, App
33	52	86.7	135	4	US-10-188-832-141	Sequence 141, App
34	52	86.7	180	4	US-10-146-473-69	Sequence 69, Appl
35	52	86.7	180	4	US-10-117-937-75	Sequence 75, Appl
36	52	86.7	180	4	US-10-296-734-834	Sequence 834, App
37	52	86.7	180	4	US-10-468-406-4	Sequence 4, Appli
38	52	86.7	180	4	US-10-657-022-75	Sequence 75, Appl
39	52	86.7	180	5	US-10-877-373-7	Sequence 7, Appli
40	52	86.7	180	6	US-11-067-064-75	Sequence 75, Appl
41	52	86.7	180	6	US-11-067-159-75	Sequence 75, Appl
42	52	86.7	210	4	US-10-157-031-88	Sequence 88, Appl
43	52	86.7	210	4	US-10-117-937-76	Sequence 76, Appl
44	52	86.7	210	4	US-10-657-022-76	Sequence 76, Appl
45	52	86.7	210	5	US-10-877-373-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-296-734-1404
; Sequence 1404, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1404
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSO1a segment 4
US-10-296-734-1404

Query Match 100.0%; Score 60; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASGPGGGAPR 11
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Db 9 RASGPGGGAPR 19

RESULT 2
US-10-482-029-202
; Sequence 202, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-202

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  Best Local Similarity   100.0%;  Pred. No. 2.3;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||| 
Db         52 RASGPGGGAPR 62


RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. US20020010321A1
;  GENERAL INFORMATION:
;    APPLICANT:  Stockert, Elisabeth; Jager, Elke;
;    APPLICANT:  Chen, Yao-tseng; Scanlan, Matthew;
;    APPLICANT:  Knuth, Alexander; Old, Lloyd J.
;    TITLE OF INVENTION:  Antibodies Which Bind to NY-ESO-1 Cancer
;    TITLE OF INVENTION:  Associated Proteins, Uses Thereof,
;    TITLE OF INVENTION:  Truncated Forms of NY-ESO-1, and HLA
;    TITLE OF INVENTION:  Binding Peptides Derived Therefrom
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/751,798
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/062,422
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/725,182
;      FILING DATE:  October 3, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. US20020010321A1man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3168
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  180
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-09-751-798-8

  Query Match             100.0%;  Score 60;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 2.3;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||| 
Db         52 RASGPGGGAPR 62


RESULT 4
US-09-849-602-30
; Sequence 30, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT:  Old, Lloyd J.
;  APPLICANT:  Stockert, Elisabeth
;  APPLICANT:  Chen, Yao-Tseng
;  TITLE OF INVENTION: Colon Cancer Antigen Panel
;  FILE REFERENCE: L0461/7105(JRV)
;  CURRENT APPLICATION NUMBER: US/09/849,602
;  CURRENT FILING DATE:  2001-05-04
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-849-602-30

  Query Match             100.0%;  Score 60;  DB 3;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 2.3;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||| 
Db         52 RASGPGGGAPR 62


RESULT 5
US-10-023-182-8
; Sequence 8, Application US/10023182
; Publication No. US20020164665A1
;   GENERAL INFORMATION:
;        APPLICANT: Stockert, Elisabeth; Jager, Elke;
;                   Chen, Yao-tseng; Scanlan, Matthew;
;                   Knuth, Alexander; Old, Lloyd J.
;        TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
;                            Associated Proteins, Uses Thereof,
;                            Truncated Forms of NY-ESO-1, and HLA
;                            Binding Peptides Derived Therefrom
;        NUMBER OF SEQUENCES: 8
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fulbright & Jaworski, L.L.P.
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10103
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: WordPerfect
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/023,182
;             FILING DATE: 17-Dec-2001
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/751,798
;             FILING DATE: December 29, 2000
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/725,182
;             FILING DATE: October 3, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, No. US20020164665A1man D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 5466.3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3168
;             TELEFAX: (212) 752-5958
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 180
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-023-182-8
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  Query Match           100.0%;  Score 60;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 2.3;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||
Db         52 RASGPGGGAPR 62


RESULT 6
US-10-207-655-71
; Sequence 71, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-207-655-71

  Query Match           100.0%;  Score 60;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 2.3;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||
Db         52 RASGPGGGAPR 62


RESULT 7
US-10-364-614-14
; Sequence 14, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
;  APPLICANT: JAGER, Elke
;  APPLICANT:  KNUTH, Alexander
;  APPLICANT:  OLD, Lloyd
;  APPLICANT:  Gnjatic, Sacha
;  TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
;  FILE REFERENCE: LUD 5726.1 CIP
;  CURRENT APPLICATION NUMBER: US/10/364,614
;  CURRENT FILING DATE:  2003-02-24
;  PRIOR APPLICATION NUMBER: US 60/355,828
;  PRIOR FILING DATE: 2002-02-13
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-364-614-14

  Query Match           100.0%;  Score 60;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 2.3;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||
Db         52 RASGPGGGAPR 62


RESULT 8
US-10-026-066-3
; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
; GENERAL INFORMATION:
;  APPLICANT: Simard, John J. L.
;  APPLICANT:  Diamond, David C.
;  TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
;  TITLE OF INVENTION:  PRESENTING CELLS
;  FILE REFERENCE: CTLIMM.21CP1C
;  CURRENT APPLICATION NUMBER: US/10/026,066
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: 09/561,074
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 09/560,465
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 09/561,572
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: 09/561,571
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: PCT/US01/13806
;  PRIOR FILING DATE: 2001-04-27
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-026-066-3

  Query Match           100.0%;  Score 60;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 2.3;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||
Db         52 RASGPGGGAPR 62


RESULT 9
US-10-117-937-74
; Sequence 74, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
;  APPLICANT: CTL IMMUNO THERAPIES CORP.
;  APPLICANT:  SIMARD, John, J.L.
;  APPLICANT:  DIAMOND, David, C.
;  APPLICANT:  LIU, Liping
;  APPLICANT:  XIE, Zhidong
;  TITLE OF INVENTION: EPITOPE SEQUENCES
;  FILE REFERENCE: CTLIMM.027A
;  CURRENT APPLICATION NUMBER: US/10/117,937
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: US 60/282,211
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: US 60/337,017
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: US 60/363,210
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 602
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-117-937-74

  Query Match           100.0%;  Score 60;  DB 4;  Length 180;
  Best Local Similarity  100.0%;  Pred. No. 2.3;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||
Db         52 RASGPGGGAPR 62


RESULT 10
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US-10-295-027-386
; Sequence 386, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 386
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-386

Query Match 100.0%; Score 60; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASGPGGGAPR 11
||||||||||||
Db 52 RASGPGGGAPR 62

RESULT 11
US-10-296-734-832
; Sequence 832, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 832
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYNSO1a consensus polypeptide
US-10-296-734-832

Query Match 100.0%; Score 60; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASGPGGGAPR 11
||||||||||||
Db 52 RASGPGGGAPR 62

RESULT 12
US-10-188-832-139
; Sequence 139, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-139

Query Match 100.0%; Score 60; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASGPGGGAPR 11
||||||||||||
Db 52 RASGPGGGAPR 62

RESULT 13
US-10-777-053-11
; Sequence 11, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANNK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07

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;  PRIOR APPLICATION NUMBER: 60/336,968
;  PRIOR FILING DATE: 2001-11-07
;  NUMBER OF SEQ ID NOS: 979
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-777-053-11
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  Query Match 100.0%; Score 60; DB 4; Length 180;
  Best Local Similarity 100.0%; Pred. No. 2.3;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 RASGPGGGAPR 11
              ||||||||||| 
Db         52 RASGPGGGAPR 62
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```
RESULT 14
US-10-751-088-15
; Sequence 15, Application US/10751088
; Publication No. US20040158044A1
;   GENERAL INFORMATION:
;        APPLICANT: Knuth, Alexader; Jager, Elke; Chen, Yao, Scanlan, Matt;
;                   Gure, Ali, Old, Lloyd, Ritter, Gerd
;        TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                            SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
;                            USES THEREOF
;        NUMBER OF SEQUENCES: 15
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FULBRIGHT & JAWORSKI LLP
;             STREET: 666 Fifth Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10158
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/751,088
;             FILING DATE: 02-Jan-2004
;             CLASSIFICATION: 530
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/165,546D
;             FILING DATE: 02-Oct-1998
;             APPLICATION NUMBER: 09/062,422
;             FILING DATE: April 17, 1998
;             APPLICATION NUMBER: 08/937,263
;             FILING DATE: September 15, 1997
;             APPLICATION NUMBER: US 08/725,182
;             FILING DATE: October 3, 1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, Norman D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 318-3000
;             TELEFAX: (212) 318-3400
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 180 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-10-751-088-15
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  Query Match 100.0%; Score 60; DB 4; Length 180;
  Best Local Similarity 100.0%; Pred. No. 2.3;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 RASGPGGGAPR 11
              ||||||||||| 
Db         52 RASGPGGGAPR 62
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RESULT 15
US-10-657-022-74
; Sequence 74, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
;  APPLICANT: Simard, John J. L.
;  APPLICANT:  Diamond, David C.
;  APPLICANT:  Liu, Liping
;  APPLICANT:  Liu, Zheng
;  TITLE OF INVENTION: EPITOPE SEQUENCES
;  FILE REFERENCE: MANNK.032A
;  CURRENT APPLICATION NUMBER: US/10/657,022
;  CURRENT FILING DATE:  2003-09-04
;  PRIOR APPLICATION NUMBER: 60/409123
;  PRIOR FILING DATE: 2002-09-06
;  NUMBER OF SEQ ID NOS: 610
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-657-022-74
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  Query Match 100.0%; Score 60; DB 4; Length 180;
  Best Local Similarity 100.0%; Pred. No. 2.3;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 RASGPGGGAPR 11
              ||||||||||| 
Db         52 RASGPGGGAPR 62
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Search completed: March 13, 2006, 20:02:27
Job time : 66.5176 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:54:06 ; Search time 7.50588 Seconds
(without alignments)
40.793 Million cell updates/sec

Title: US-09-529-206E-30
Perfect score: 60
Sequence: 1 RASGPGGGAPR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	60	100.0	180	7	US-11-155-288-7	Sequence 7, Appli
2	60	100.0	240	7	US-11-021-441-28	Sequence 28, Appl
3	48	80.0	20	6	US-10-623-155-496	Sequence 496, App
4	45	75.0	678	7	US-11-072-512-3295	Sequence 3295, Ap
5	43	71.7	306	7	US-11-096-568A-20556	Sequence 20556, A
6	42	70.0	134	7	US-11-096-568A-23806	Sequence 23806, A
7	41	68.3	365	7	US-11-108-528-58	Sequence 58, Appl
8	41	68.3	537	7	US-11-179-958A-2	Sequence 2, Appli
9	41	68.3	555	7	US-11-072-512-3369	Sequence 3369, Ap
10	41	68.3	953	7	US-11-037-243-66	Sequence 66, Appl
11	40.5	67.5	280	7	US-11-143-980-34	Sequence 34, Appl
12	40	66.7	558	7	US-11-096-568A-26217	Sequence 26217, A
13	40	66.7	974	6	US-10-531-036-35	Sequence 35, Appl
14	40	66.7	1832	7	US-11-087-099-7762	Sequence 7762, Ap
15	39	65.0	213	7	US-11-072-512-2722	Sequence 2722, Ap
16	39	65.0	233	7	US-11-240-769-58	Sequence 58, Appl
17	39	65.0	353	7	US-11-096-568A-22334	Sequence 22334, A
18	39	65.0	358	7	US-11-096-568A-22333	Sequence 22333, A
19	39	65.0	413	7	US-11-096-568A-27265	Sequence 27265, A
20	39	65.0	420	7	US-11-096-568A-22332	Sequence 22332, A
21	39	65.0	430	6	US-10-992-577-8	Sequence 8, Appli
22	39	65.0	430	6	US-10-508-892-2	Sequence 2, Appli
23	39	65.0	430	7	US-11-223-294-54	Sequence 54, Appl
24	39	65.0	618	7	US-11-078-735-18	Sequence 18, Appl
25	39	65.0	618	7	US-11-050-346-63	Sequence 63, Appl
26	39	65.0	618	7	US-11-103-077-18	Sequence 18, Appl
27	39	65.0	662	7	US-11-072-175-184	Sequence 184, App
28	38	63.3	132	7	US-11-096-568A-14323	Sequence 14323, A
29	38	63.3	228	7	US-11-096-568A-16457	Sequence 16457, A
30	38	63.3	236	7	US-11-096-568A-22845	Sequence 22845, A
31	38	63.3	274	7	US-11-096-568A-22603	Sequence 22603, A
32	38	63.3	306	7	US-11-096-568A-12071	Sequence 12071, A
33	38	63.3	320	7	US-11-096-568A-988	Sequence 988, App
34	38	63.3	438	6	US-10-650-326B-9	Sequence 9, Appli
35	38	63.3	459	7	US-11-096-568A-21887	Sequence 21887, A
36	38	63.3	1121	7	US-11-087-099-9800	Sequence 9800, Ap
37	38	63.3	1121	7	US-11-087-099-11165	Sequence 11165, A
38	37	61.7	152	7	US-11-096-568A-342	Sequence 342, App
39	37	61.7	167	7	US-11-096-568A-10542	Sequence 10542, A
40	37	61.7	189	7	US-11-107-029-4	Sequence 4, Appli
41	37	61.7	198	7	US-11-096-568A-22494	Sequence 22494, A
42	37	61.7	269	7	US-11-096-568A-22493	Sequence 22493, A
43	37	61.7	328	7	US-11-096-568A-11283	Sequence 11283, A
44	37	61.7	375	7	US-11-096-568A-24377	Sequence 24377, A
45	37	61.7	379	7	US-11-109-156-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-11-155-288-7
; Sequence 7, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-7

Query Match 100.0%; Score 60; DB 7; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASGPGGGAPR 11
||||||||||||
Db 52 RASGPGGGAPR 62

RESULT 2
US-11-021-441-28
; Sequence 28, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06

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;  PRIOR APPLICATION NUMBER: US 60/615,287
;  PRIOR FILING DATE: 2004-10-01
;  PRIOR APPLICATION NUMBER: US 60/599,377
;  PRIOR FILING DATE: 2004-08-05
;  PRIOR APPLICATION NUMBER: PCT/US2004/23881
;  PRIOR FILING DATE: 2004-07-23
;  PRIOR APPLICATION NUMBER: US 10/883,599
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: US 60/556,744
;  PRIOR FILING DATE: 2004-03-26
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion protein
US-11-021-441-28

  Query Match             100.0%;  Score 60;  DB 7;  Length 240;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              ||||||||||
Db        112 RASGPGGGAPR 122


RESULT 3
US-10-623-155-496
; Sequence 496, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Peckham, David W.
;  APPLICANT:  Retteť, Marc W.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C20
;  CURRENT APPLICATION NUMBER: US/10/623,155
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 496
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-623-155-496

  Query Match             80.0%;  Score 48;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGA 9
              |||||||||
Db         12 RASGPGGGA 20


RESULT 4
US-11-072-512-3295
; Sequence 3295, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
;  APPLICANT: ISOGAI, TAKAO
;  APPLICANT:  SUGIYAMA, TOMOYASU
;  APPLICANT:  OTSUKI, TETSUJI
;  APPLICANT:  WAKAMATSU, AI
;  APPLICANT:  SATO, HIROYUKI
;  APPLICANT:  ISHII, SHIZUKO
;  APPLICANT:  YAMAMOTO, JUN-ICHI
;  APPLICANT:  ISONO, YUUKO
;  APPLICANT:  HIO, YURI
;  APPLICANT:  OTSUKA, KAORU
;  APPLICANT:  NAGAI, KEIICHI
;  APPLICANT:  IRIE, RYOTARO
;  APPLICANT:  TAMECHIKA, ICHIRO
;  APPLICANT:  SEKI, NAOHIKO
;  APPLICANT:  YOSHIKAWA, TSUTOMU
;  APPLICANT:  OTSUKA, MOTOYUKI
;  APPLICANT:  NAGAHARI, KENJI
;  APPLICANT:  MASUHO, YASUHIKO
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: 084335-0191
;  CURRENT APPLICATION NUMBER: US/11/072,512
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: US 60/350,978
;  PRIOR FILING DATE: 2002-01-25
;  PRIOR APPLICATION NUMBER: JP 2001-379298
;  PRIOR FILING DATE: 2001-11-05
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3295
;   LENGTH: 678
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-072-512-3295

  Query Match             75.0%;  Score 45;  DB 7;  Length 678;
  Best Local Similarity   80.0%;  Pred. No. 30;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAP 10
              ||:||||| |
Db        592 RAAGPGGGWP 601


RESULT 5
US-11-096-568A-20556
; Sequence 20556, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20556
;   LENGTH: 306
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(306)
;   OTHER INFORMATION: Ceres Seq. ID no. 12383286
US-11-096-568A-20556

  Query Match             71.7%;  Score 43;  DB 7;  Length 306;
  Best Local Similarity   80.0%;  Pred. No. 29;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAP 10
              || ||| |||
Db         92 RADGPGTGAP 101


RESULT 6
US-11-096-568A-23806
; Sequence 23806, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
```

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;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23806
;   LENGTH: 134
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(134)
;   OTHER INFORMATION: Ceres Seq. ID no. 12415289
US-11-096-568A-23806

  Query Match            70.0%;  Score 42;  DB 7;  Length 134;
  Best Local Similarity  70.0%;  Pred. No. 19;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAP 10
              | :||| |||
Db         70 RGAGPGAGAP 79


RESULT 7
US-11-108-528-58
; Sequence 58, Application US/11108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
;  APPLICANT: Larsen, Glenn
;  APPLICANT:  Marvin, Martha
;  APPLICANT:  Li, Dean Y.
;  APPLICANT:  Wang, Elizabeth
;  APPLICANT:  Chen, C. M. Amy
;  APPLICANT:  Shamah, Steven M.
;  TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
;  TITLE OF INVENTION:  PROLIFERATION
;  FILE REFERENCE: HYDR-P01-041
;  CURRENT APPLICATION NUMBER: US/11/108,528
;  CURRENT FILING DATE:  2005-04-18
;  PRIOR APPLICATION NUMBER: US 60/563,137
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 60/598,368
;  PRIOR FILING DATE: 2004-08-02
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 58
;   LENGTH: 365
;   TYPE: PRT
;   ORGANISM: Mouse
US-11-108-528-58

  Query Match            68.3%;  Score 41;  DB 7;  Length 365;
  Best Local Similarity  80.0%;  Pred. No. 62;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAP 10
              |||| ||| |
Db        273 RASGSGGGDP 282


RESULT 8
US-11-179-958A-2
; Sequence 2, Application US/11179958A
; Publication No. US20060030537A1
; GENERAL INFORMATION:
;  APPLICANT: Chalfant, Charles E.
;  APPLICANT:  Hannun, Yusef A.
;  APPLICANT:  Pettus, Benjamin J.
;  APPLICANT:  Bielawska, Alicja
;  TITLE OF INVENTION: Ceramide Kinase and Uses Thereof
;  FILE REFERENCE: 9175-028-999 (MUSC Ref P0401)
;  CURRENT APPLICATION NUMBER: US/11/179,958A
;  CURRENT FILING DATE:  2005-07-11
;  PRIOR APPLICATION NUMBER: 60/586,909
;  PRIOR FILING DATE: 2004-07-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 537
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Human ceramide kinase
US-11-179-958A-2

  Query Match            68.3%;  Score 41;  DB 7;  Length 537;
  Best Local Similarity  70.0%;  Pred. No. 86;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAP 10
              |: ||| |||
Db         36 RSPGPGAGAP 45


RESULT 9
US-11-072-512-3369
; Sequence 3369, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
;  APPLICANT: ISOGAI, TAKAO
;  APPLICANT:  SUGIYAMA, TOMOYASU
;  APPLICANT:  OTSUKI, TETSUJI
;  APPLICANT:  WAKAMATSU, AI
;  APPLICANT:  SATO, HIROYUKI
;  APPLICANT:  ISHII, SHIZUKO
;  APPLICANT:  YAMAMOTO, JUN-ICHI
;  APPLICANT:  ISONO, YUUKO
;  APPLICANT:  HIO, YURI
;  APPLICANT:  OTSUKA, KAORU
;  APPLICANT:  NAGAI, KEIICHI
;  APPLICANT:  IRIE, RYOTARO
;  APPLICANT:  TAMECHIKA, ICHIRO
;  APPLICANT:  SEKI, NAOHIKO
;  APPLICANT:  YOSHIKAWA, TSUTOMU
;  APPLICANT:  OTSUKA, MOTOYUKI
;  APPLICANT:  NAGAHARI, KENJI
;  APPLICANT:  MASUHO, YASUHIKO
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: 084335-0191
;  CURRENT APPLICATION NUMBER: US/11/072,512
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: US 60/350,978
;  PRIOR FILING DATE: 2002-01-25
;  PRIOR APPLICATION NUMBER: JP 2001-379298
;  PRIOR FILING DATE: 2001-11-05
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3369
;   LENGTH: 555
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-072-512-3369

  Query Match            68.3%;  Score 41;  DB 7;  Length 555;
  Best Local Similarity  77.8%;  Pred. No. 88;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ASGPGGGAP 10
              ||||| |:|
Db        473 ASGPGSGSP 481


RESULT 10
US-11-037-243-66
; Sequence 66, Application US/11037243
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; Publication No. US20050287546A1
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY
;  APPLICANT:  WHYTE, DAVID
;  APPLICANT:  CAENEPEEL, SEAN
;  APPLICANT:  CHARYDCZAK, GLEN
;  APPLICANT:  MANNING, GERARD
;  APPLICANT:  SUDARSANAM, SUCHA
;  TITLE OF INVENTION: NOVEL PROTEASES
;  FILE REFERENCE: 038602/1214
;  CURRENT APPLICATION NUMBER: US/11/037,243
;  CURRENT FILING DATE:  2005-05-26
;  PRIOR APPLICATION NUMBER: US/09/888,615
;  PRIOR FILING DATE: 2001-06-26
;  PRIOR APPLICATION NUMBER: 60/214,047
;  PRIOR FILING DATE: 2000-06-26
;  NUMBER OF SEQ ID NOS: 150
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
;   LENGTH: 953
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-037-243-66

  Query Match             68.3%;  Score 41;  DB 7;  Length 953;
  Best Local Similarity   87.5%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GPGGGAPR 11
              ||||| ||
Db        214 GPGGGHPR 221


RESULT 11
US-11-143-980-34
; Sequence 34, Application US/11143980
; Publication No. US20050272133A1
; GENERAL INFORMATION:
;  APPLICANT: He, Min
;  APPLICANT:  Hucul, John
;  APPLICANT:  Haltli, Bradley A.
;  APPLICANT:  Wagenaar, Melissa M.
;  APPLICANT:  Graziani, Edmund
;  APPLICANT:  Summers, Mia
;  APPLICANT:  Kulowski, Kerry
;  APPLICANT:  Pong, Kevin
;  TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex
;  TITLE OF INVENTION:  Polyketide
;  FILE REFERENCE: AM-101426US
;  CURRENT APPLICATION NUMBER: US/11/143,980
;  CURRENT FILING DATE:  2005-06-03
;  PRIOR APPLICATION NUMBER: US 60/664,483
;  PRIOR FILING DATE: 2005-03-23
;  PRIOR APPLICATION NUMBER: US 60/576,895
;  PRIOR FILING DATE: 2004-06-03
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
;   LENGTH: 280
;   TYPE: PRT
;   ORGANISM: Streptomyces sp.
US-11-143-980-34

  Query Match             67.5%;  Score 40.5;  DB 7;  Length 280;
  Best Local Similarity   75.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 RASGPGG-GAPR 11
              | ||||| | ||
Db        116 RPSGPGGPGGPR 127


RESULT 12
US-11-096-568A-26217
; Sequence 26217, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26217
;   LENGTH: 558
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(558)
;   OTHER INFORMATION: Ceres Seq. ID no. 13498878
US-11-096-568A-26217

  Query Match             66.7%;  Score 40;  DB 7;  Length 558;
  Best Local Similarity   63.6%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 RASGPGGGAPR 11
              |  || || ||
Db        390 RQEGPAGGEPR 400


RESULT 13
US-10-531-036-35
; Sequence 35, Application US/10531036
; Publication No. US20060015951A1
; GENERAL INFORMATION:
;  APPLICANT: Eulenberg, Karsten
;  APPLICANT:  Meise, Martin
;  APPLICANT:  Molitor, Andreas
;  APPLICANT:  Steuernagel, Arnd
;  TITLE OF INVENTION: Proteins Involved in the Regulation of Energy Homeostasis
;  FILE REFERENCE: 2923-696
;  CURRENT APPLICATION NUMBER: US/10/531,036
;  CURRENT FILING DATE:  2005-04-12
;  PRIOR APPLICATION NUMBER: PCT/EP03/11352
;  PRIOR FILING DATE: 2003-10-14
;  PRIOR APPLICATION NUMBER: EP 02024747.4
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: EP 02023560.2
;  PRIOR FILING DATE: 2002-10-22
;  PRIOR APPLICATION NUMBER: EP 02022880.5
;  PRIOR FILING DATE: 2002-10-14
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
;   LENGTH: 974
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-531-036-35

  Query Match             66.7%;  Score 40;  DB 6;  Length 974;
  Best Local Similarity   75.0%;  Pred. No. 1.9e+02;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    1;

Qy          1 RASG--PGGGAP 10
              || |  ||||||
Db          6 RAGGPPPGGGAP 17


RESULT 14
US-11-087-099-7762
; Sequence 7762, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
```

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;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7762
;   LENGTH: 1832
;   TYPE: PRT
;   ORGANISM: Podospora anserina
US-11-087-099-7762

  Query Match             66.7%;  Score 40;  DB 7;  Length 1832;
  Best Local Similarity   77.8%;  Pred. No. 3.3e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 SGPGGGAPR 11
              || |||:||
Db       1051 SGSGGGSPR 1059


RESULT 15
US-11-072-512-2722
; Sequence 2722, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
;  APPLICANT: ISOGAI, TAKAO
;  APPLICANT:  SUGIYAMA, TOMOYASU
;  APPLICANT:  OTSUKI, TETSUJI
;  APPLICANT:  WAKAMATSU, AI
;  APPLICANT:  SATO, HIROYUKI
;  APPLICANT:  ISHII, SHIZUKO
;  APPLICANT:  YAMAMOTO, JUN-ICHI
;  APPLICANT:  ISONO, YUUKO
;  APPLICANT:  HIO, YURI
;  APPLICANT:  OTSUKA, KAORU
;  APPLICANT:  NAGAI, KEIICHI
;  APPLICANT:  IRIE, RYOTARO
;  APPLICANT:  TAMECHIKA, ICHIRO
;  APPLICANT:  SEKI, NAOHIKO
;  APPLICANT:  YOSHIKAWA, TSUTOMU
;  APPLICANT:  OTSUKA, MOTOYUKI
;  APPLICANT:  NAGAHARI, KENJI
;  APPLICANT:  MASUHO, YASUHIKO
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: 084335-0191
;  CURRENT APPLICATION NUMBER: US/11/072,512
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: US 60/350,978
;  PRIOR FILING DATE: 2002-01-25
;  PRIOR APPLICATION NUMBER: JP 2001-379298
;  PRIOR FILING DATE: 2001-11-05
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2722
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-072-512-2722

  Query Match             65.0%;  Score 39;  DB 7;  Length 213;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 SGPGGGA 9
              |||||||
Db         56 SGPGGGA 62


Search completed: March 13, 2006, 20:03:31
Job time : 7.50588 secs
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